EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	28	simulat$ near10 (microarray or (micro adj array))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/06/19 18:39
L2	832	computer$ near10 (microarray or (micro adj array))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/06/19 18:39
L3	858	l1 or l2	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/06/19 18:40
L4	3655	435/91.1[ccls]	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/06/19 18:42
L5	35987	435/6[ccls]	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/06/19 18:42
L6	2600	702/19[ccls]	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/06/19 18:42
L7	1699	702/20[ccls]	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/06/19 18:42
L8	39205	l4 or l5 or l6 or l7	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/06/19 18:43
L9	31175	l3 an dl8	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/06/19 18:43

EAST Search Hist ry

L10	436	l3 and l8	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/06/19 18:43
L11	1136024	@rlad<"20030121"	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/06/19 18:43
L12	244	l10 and l11	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/06/19 18:43

Serial No. 10/501,848

Please scan these and index them as

"Examiner Search Notes"

Thank you.

James Martinell
Primary Examiner 1634

```
********** Welcome to STN International **********

 NEWS 1       Web Page URLs for STN Seminar Schedule - N. America
 NEWS 2       "Ask CAS" for self-help around the clock
 NEWS 3 JAN 17 Pre-1988 INPI data added to MARPAT
 NEWS 4 FEB 21 STN AnaVist, Version 1.1, lets you share your STN AnaVist
visualization results
 NEWS 5 FEB 22 The IPC thesaurus added to additional patent databases on STN
 NEWS 6 FEB 22 Updates in EPFULL; IPC 8 enhancements added
 NEWS 7 FEB 27 New STN AnaVist pricing effective March 1, 2006
 NEWS 8 MAR 03 Updates in PATDPA; addition of IPC 8 data without attributes
 NEWS 9 MAR 22 EMBASE is now updated on a daily basis
 NEWS 10 APR 03 New IPC 8 fields and IPC thesaurus added to PATDPAFULL
 NEWS 11 APR 03 Bibliographic data updates resume; new IPC 8 fields and IPC
thesaurus added in PCTFULL
 NEWS 12 APR 04 STN AnaVist $500 visualization usage credit offered
 NEWS 13 APR 12 LINSPEC, learning database for INSPEC, reloaded and enhanced
 NEWS 14 APR 12 Improved structure highlighting in FQHIT and QHIT display
in MARPAT
 NEWS 15 APR 12 Derwent World Patents Index to be reloaded and enhanced during
second quarter; strategies may be affected
 NEWS 16 MAY 10 CA/CAplus enhanced with 1900-1906 U.S. patent records
 NEWS 17 MAY 11 KOREAPAT updates resume
 NEWS 18 MAY 19 Derwent World Patents Index to be reloaded and enhanced
 NEWS 19 MAY 30 IPC 8 Rolled-up Core codes added to CA/CAplus and
USPATFULL/USPAT2
 NEWS 20 MAY 30 The F-Term thesaurus is now available in CA/CAplus
 NEWS 21 JUN 02 The first reclassification of IPC codes now complete in
INPADOC

 NEWS EXPRESS JUNE 16 CURRENT WINDOWS VERSION IS V8.01b, CURRENT
MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),          AND CURRENT
DISCOVER FILE IS DATED 23 MAY 2006.

 NEWS HOURS   STN Operating Hours Plus Help Desk Availability
 NEWS LOGIN   Welcome Banner and News Items
 NEWS IPC8    For general information regarding STN implementation of IPC 8
 NEWS X25     X.25 communication option no longer available after June 2006

Enter NEWS followed by the item number or name to see news on that
specific topic.

  All use of STN is subject to the provisions of the STN Customer
  agreement. Please note that this agreement limits use to scientific
  research. Use for software development or design or implementation
  of commercial gateways or other similar uses is prohibited and may
  result in loss of user privileges and other penalties.

********** STN Columbus **********

FILE 'HOME' ENTERED AT 18:48:15 ON 19 JUN 2006

=> file caplus
COST IN U.S. DOLLARS                    SINCE FILE     TOTAL
ENTRY    SESSION
FULL ESTIMATED COST                        0.21       0.21

FILE 'CAPLUS' ENTERED AT 18:48:28 ON 19 JUN 2006
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2006 AMERICAN CHEMICAL SOCIETY (ACS)


Copyright of the articles to which records in this database refer is
held by the publishers listed in the PUBLISHER (PB) field (available
for records published or updated in Chemical Abstracts after December
26, 1996), unless otherwise indicated in the original publications.
The CA Lexicon is the copyrighted intellectual property of the
American Chemical Society and is provided to assist you in searching
databases on STN. Any dissemination, distribution, copying, or storing
of this information, without the prior written consent of CAS, is
strictly prohibited.

FILE COVERS 1907 - 19 Jun 2006 VOL 144 ISS 26
FILE LAST UPDATED: 18 Jun 2006 (20060618/ED)

Effective October 17, 2005, revised CAS Information Use Policies apply.
They are available for your review at:

http://www.cas.org/infopolicy.html

=> s (simulat?(10a)(microarray# or (micro(w)array#)))/bi,ab
UNMATCHED LEFT PARENTHESIS '(SIMULAT?'
The number of right parentheses in a query must be equal to the
number of left parentheses.

=> s (simulat?(10a)(microarray# or (micro(w)array#)))/bi,ab    746182 SIMULAT?/BI
427790 SIMULAT?/AB              40727 MICROARRAY#/BI              22794
MICROARRAY#/AB              154958 MICRO/BI              93105 MICRO/AB
145099 ARRAY#/BI              134850 ARRAY#/AB
L1       341 (SIMULAT?(10A)(MICROARRAY# OR (MICRO(W)ARRAY#)))/BI,AB

=> s (computer?(10a)(microarray# or (micro(w)array#)))/bi,ab    293456
COMPUTER?/BI              207478 COMPUTER?/AB              40727
MICROARRAY#/BI              22794 MICROARRAY#/AB              154958
MICRO/BI              93105 MICRO/AB              145099 ARRAY#/BI
134850 ARRAY#/AB
L2       641 (COMPUTER?(10A)(MICROARRAY# OR (MICRO(W)ARRAY#)))/BI,AB

=> s l1 or l2
L3       929 L1 OR L2

=> s l3 not 2006/py    572333 2006/PY
L4       859 L3 NOT 2006/PY

=> s l4 not 2005/py    1278142 2005/PY
L5       611 L4 NOT 2005/PY

=> s l5 not 2004/py    1291977 2004/PY
L6       407 L5 NOT 2004/PY

=> d his
 (FILE 'HOME' ENTERED AT 18:48:15 ON 19 JUN 2006)
 FILE 'CAPLUS' ENTERED AT 18:48:28 ON 19 JUN 2006
L1       341 S (SIMULAT?(10A)(MICROARRAY# OR (MICRO(W)ARRAY#)))/BI,AB
L2       641 S (COMPUTER?(10A)(MICROARRAY# OR (MICRO(W)ARRAY#)))/BI,AB
L3       929 S L1 OR L2
L4       859 S L3 NOT 2006/PY
L5       611 S L4 NOT 2005/PY
L6       407 S L5 NOT 2004/PY


=> d l6 1-407 bib ab

L6  ANSWER 1 OF 407  CAPLUS  COPYRIGHT 2006 ACS on STN
AN  2005:629351  CAPLUS
DN  143:147283
TI  Optimal design of single factor cDNA microarray experiments and mixed models for
gene expression data
AU  Yang, Xiao
CS  Virginia Polytechnic Institute and State Univ., Blacksburg, VA, USA
SO  (2003) 98 pp. Avail.: UMI, Order No. DA3141112 From: Diss. Abstr. Int., B 2005,
65(7), 3529
DT  Dissertation
LA  English
AB  Unavailable

L6  ANSWER 2 OF 407  CAPLUS  COPYRIGHT 2006 ACS on STN
AN  2005:481472  CAPLUS
DN  143:127766
TI  Data analysis tools for DNA microarrays
AU  Draghici, Sorin
CS  USA
SO  (2003) Publisher: (Chapman & Hall/CRC, Boca Raton, Fla.), 512 pp. ISBN: 1-
58488-315-4
DT  Book
LA  English
AB  Unavailable

L6  ANSWER 3 OF 407  CAPLUS  COPYRIGHT 2006 ACS on STN
AN  2005:213730  CAPLUS
DN  143:54373
TI  DNA Microarrays and Gene Expression: From Experience to Data Analysis and
Modeling
AU  Baldi, Pierre; Hatfield, G. Wesley
CS  UK
SO  (2002) Publisher: (Cambridge University Press, Cambridge, UK), 200 pp. ISBN: 0-
521-80022-6
DT  Book
LA  English
AB  Unavailable

L6  ANSWER 4 OF 407  CAPLUS  COPYRIGHT 2006 ACS on STN
AN  2005:131600  CAPLUS
DN  143:24559
TI  Effects of CpG oligodeoxynucleotide on gene expression in immunocytes
AU  Hu, Zhenlin; Wan, Bin; Zhou, Fengjuan; Wang, Jing; Wang, Qingmin; Sun, Shuhan
CS  Department of Medical Genetics, College of Basic Medical Sciences, Second Military
Medical University, Shanghai, 200433, Peop. Rep. China
SO  Dier Junyi Daxue Xuebao (2003), 24(10), 1086-1089 CODEN: DJXUE5; ISSN:
0258-879X
PB  Dier Junyi Daxue Xuebao Bianjibu
DT  Journal
LA  Chinese
AB  The influence of CpG oligodeoxynucleotide (CpG-ODN) on the gene expression in
immunocytes and its mechanisms were studied. RAW264.7 cells were stimulated with
CpG-ODN for 6 h, and mRNA from both control and treated cells were isolated and
```

purified, then were reversely transcribed to cDNA with the incorporation of fluorescent-labeled dUTP to prep. the hybridization probes. The mixed probes were then hybridized to the cDNA microarray MGEC-80s. After high-stringent washing, the cDNA ***microarray*** was scanned by ***computer*** system and the differently expressed genes were obtained. A total of 119 differently expressed genes were detected after CpG-ODN stimulation, of which 74 were up-regulated and 45 were down-regulated. These genes were related to cell cycle, immune modulation, lipid metab., foam cell formation, and signal transduction. CpG-UDN may widely modulate the expression of many genes in immune cells, and further anal. of related genes may help understand the mol. mechanisms of CpG-ODN.

L6 ANSWER 5 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:980924 CAPLUS
DN 142:149687
TI Arrays of oligonucleotide probes for digital recognition by computer
IN Jin, Dong Gyu
PA Cosmogenome Inc., S. Korea
SO Repub. Korean Kongkae Taeho Kongbo, No pp. given CODEN: KRXXA7
DT Patent
LA Korean
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI KR 2003060907 A 20030716 KR 2003-705129 20030411
PRAI KR 2003-705129 20030411
AB Arrays of oligonucleotide probes for digital recognition by a computer are provided, thereby easily and rapidly interpreting the anal. results of dots in a chip. An array of oligonucleotide, probes on a solid support for detecting the point mutation of testee's DNA sample comprises (i) a labeling part of arrays including catalog no., gene sequence no., ID no., command and IP address, which indicates information for sample DNA identification to be read by a computer; and (ii) a logic part of arrays including arrays of probes in 4 columns in at least 100 up to 100,000 rows, wherein each column consists of 2 symbols, that are, a control symbol having a detectible marker for digital recognition by a computer and hybridization symbol comprising oligonucleotide probes in the 5 to 30 nucleotides length occupying known sites by substituting target oligonucleotide into ACGT in each column.

L6 ANSWER 6 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:947551 CAPLUS
DN 143:282023
TI Computer simulation system of DNA-binding protein experiment based on dsDNA microassay
AU Xie, Jianming; Bai, Yunfei; Qian, Lulu; Cui, Lei; Sun, Xiao; Lu, Zuhong
CS Chien-Shiung Wu Laboratory, Southeast University, Nanjing, 210096, Peop. Rep. China
SO Shengwu Wuli Xuebao (2003), 19(2), 156-160 CODEN: SWXUEN; ISSN: 1000-6737
PB Shengwu Wuli Xuebao Bianjibu
DT Journal
LA Chinese
AB D5DNA (double-stranded DNA) microarray, as a novel high-throughout technique, get a start in the field of DNA-binding protein research. It studied a dsDNA probe designing method for a new fabrication technol. of the dsDNA microarray. T. Hen a computer software named 'DBP' was introduced, which ***simulated*** the procedures of DNA-binding protein expt. based on dsDNA ***microarray*** and included DNA digestion using restriction enzymes, electrophoresis, hybridization and data management. Using DBP software, it can design dsDNA probes give advice on expt. planning and predictive results of a DNA-binding protein expt.

L6 ANSWER 7 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:938025 CAPLUS
DN 142:211570
TI Effect of .beta.-carotene on gene expression of breast cancer cells
AU Li, Zhong; Hu, Chunyan; Mo, Baoqing; Xu, Jida; Zhao, Yan
CS Department of Nutrition and Food Science, Nanjing Medical University, Nanjing, Jiangsu Province, 210029, Peop. Rep. China
SO Aizheng (2003), 22(4), 380-384 CODEN: AIZHE4; ISSN: 1000-467X
PB Sun Yat-sen Daxue, Aizheng Zhongxin
DT Journal
LA Chinese
AB Study the altered gene expression of MCF-7 cell before and after the treatment with .beta.-carotene using cDNA microarray and the mechanism that .beta.-carotene induce breast cancer cell apoptosis. Two fluorescence cDNA probes were made using reverse transcription reaction from mRNA of .beta.-carotene untreated or treated MCF-7 cells (human estrogen receptor pos. breast cancer cells), marked with two different fluorescence dyes (cy3 and cy5) resp., hybridized with expressed cDNA ***microarray*** scanned and analyzed by ***computer*** system and finally the expressed gene was produced. A total of 21 genes related to cell apoptosis, cell signal transduction, protein translation and immunity were expressed differently after the treatment of .beta.-carotene, which 3/21 were up-regulated (AF040958, AK001555, g41894), 18/21 were down-regulated (hshsp90r, U83857, AB014509, AF126028, AF053641, AF117386, AF050127, NM_012177, humtopi, AJ250915, U37547, U78798, NM_004849, NM_005346, af004711, NM_006595, NM_001418, AB015051). The results suggested that .beta.-carotene might inhibit the growth of breast cancer cells through inducing apoptosis, breaking signal transduction, and blocking protein translation.

L6 ANSWER 8 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:800698 CAPLUS
DN 142:149649
TI Multiclass classification of microarray data with repeated measurements: application to cancer
AU Yeung, Ka Yee; Bumgarner, Roger E.
CS Department of Microbiology, University of Washington, Seattle, WA, 98195, USA
SO GenomeBiology (2003), 4(12), No pp. given CODEN: GNBLFW; ISSN: 1465-6914
URL: http://genomebiology.com/content/pdf/gb-2003-4-12-r83.pdf
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Prediction of the diagnostic category of a tissue sample from its gene-expression profile and selection of relevant genes for class prediction have important applications in cancer research. We have developed the uncorrelated shrunken centroid (USC) and error-weighted, uncorrelated shrunken centroid (EWUSC) algorithms that are applicable to microarray data with any no. of classes. We show that removing highly correlated genes typically improves classification results using a small set of genes.
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 9 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:800097 CAPLUS
DN 142:149274
TI Application of independent component analysis to microarrays
AU Lee, Su-In; Batzoglou, Serafim
CS Dep. Electrical Eng., Stanford Univ., Stanford, CA, 94305-9010, USA
SO GenomeBiology (2003), 4(11), No pp. given CODEN: GNBLFW; ISSN: 1465-6914
URL: http://genomebiology.com/content/pdf/gb-2003-4-11-r76.pdf
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB We apply linear and nonlinear independent component anal. (ICA) to project microarray data into statistically independent components that correspond to putative biol. processes, and to cluster genes according to over- or under-expression in each component. We test the statistical significance of enrichment of gene annotations within clusters. ICA outperforms other leading methods, such as principal component anal., k-means clustering and the Plaid model, in constructing functionally coherent clusters on microarray datasets from Saccharomyces cerevisiae, Caenorhabditis elegans and human.
RE.CNT 75 THERE ARE 75 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 10 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:719122 CAPLUS
DN 141:201243
TI Visualization of gene expression data - the GE-biplot, the chip-plot and the gene-plot
AU Pittelkow, Yvonne E.; Wilson, Susan R.
CS Australian Natl. Univ., Australia
SO Statistical Applications in Genetics and Molecular Biology (2003), 2(1), No pp. given CODEN: SAGMCU; ISSN: 1544-6115 URL: http://www.bepress.com/cgi/viewcontent.cgi?article=1019&context=sagmb
PB Berkeley Electronic Press
DT Journal; (online computer file)
LA English
AB Visualization methods for exploring microarray data are particularly important for gaining insight into data from gene expression expts., such as those concerned with the development of an understanding of gene function and interactions. Further, good visualization techniques are useful for outlier detection in microarray data and for aiding biol. interpretation of results, as well as for presentation of overall summaries of the data. The biplot is particularly useful for the display of microarray data as both the genes and the chips can be simultaneously plotted. In this paper we describe several ordination techniques suitable for exploring microarray data, and we call these the GE-biplot, the Chip-plot and the Gene-plot. The general method is first evaluated on synthetic data ***simulated*** in accord with current biol. interpretation of ***microarray*** data. Then it is applied to two well-known data sets, namely the colon data of Alon et al. (1999) and the leukemia data of Golub et al. (1999). The usefulness of the approach for interpreting and comparing different analyses of the same data is demonstrated.
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 11 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:623389 CAPLUS
DN 142:310444
TI Improving the specificity of biological signal detection from microarray data
AU Troyanskaya, Olga G.
CS Stanford Univ., Stanford, CA, USA
SO (2003) 118 pp. Avail.: UMI, Order No. DA3104167 From: Diss. Abstr. Int., B 2004, 64(9), 4181
DT Dissertation
LA English
AB Unavailable

L6 ANSWER 12 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:572371 CAPLUS
DN 141:200855
TI Probabilistic estimation of microarray data reliability and underlying gene expression
AU Bilke, S.; Breslin, T.; Sigvardsson, M.

CS Complex Systems Division, Department of Theoretical Physics, University of Lund, Lund, SE-22185, Swed.
SO Los Alamos National Laboratory, Preprint Archive, Quantitative Biology (2003) 1-12, arXiv:q-bio.QM/0309006, 18 Sep 2003 CODEN: LANLCJ URL: http://xxx.lanl.gov/pdf/q-bio.QM/0309006
PB Los Alamos National Laboratory
DT Preprint
LA English
AB The availability of high throughput methods for measurement of mRNA concns. makes the reliability of conclusions drawn from the data and global quality control of samples and hybridization important issues. These issues were addressed by an information theoretic approach, applied to discretized expression values in replicated gene expression data. The approach yields a quant. measure of two important parameter classes: First, the probability P(.sigma.|S) that a gene is in the biol. state .sigma. in a certain variety, given its obsd. expression S in the samples of that variety. Second, sample specific error probabilities which serve as consistency indicators of the measured samples of each variety. The method and its limitations are tested on gene expression data for developing murine B-cells and a t-test is used as ref. On a set of known genes it performs better than the t-test despite the crude discretization into only two expression levels. The consistency indicators, i.e. the error probabilities, correlate well with variations in the biol. material and thus prove efficient. The proposed method is effective in detg. differential gene expression and sample reliability in replicated microarray data. Already at two discrete expression levels in each sample, it gives a good explanation of the data and is comparable to std. techniques.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 13 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:567994 CAPLUS
DN 141:272143
TI Evaluation of sensitivity, performance and reproducibility of microarray technology in neuronal tissue
AU Evans, S. J.; Watson, S. J.; Akil, H.
CS Mental Health Research Institute, University of Michigan, Ann Arbor, MI, 48109, USA
SO Integrative and Comparative Biology (2003), 43(6), 780-785 CODEN: ICBNBD; ISSN: 1540-7063
PB Society for Integrative and Comparative Biology
DT Journal
LA English
AB Microarray technol. is a powerful technique that allows the simultaneous study of thousands of gene transcripts. During the past two years there has been an explosion of publications describing expts. utilizing microarray technol. that range from original research findings from biol. paradigms to math. modeled systems. However, neuroscientists using microarray technol. face significant challenges due to high tissue complexity, low abundance transcripts, and small magnitude changes in transcript levels that have significant biol. impact. This manuscript describes a series of studies designed to address issues regarding microarray sensitivity, ability of microarrays to detect subtle changes, and reproducibility of microarray expts., all in the context of neuronal tissue. From the presentation of these studies, the authors argue that although microarray technol. is limited with regards to sensitivity, the outcome of these expts., if approached with appropriate skepticism, can be fruitful in the generation of hypotheses and seeding of future expts.
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 14 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:532664 CAPLUS
DN 141:406692
TI On bayesian modeling and design for microarray gene expression data
AU Ji, Yuan
CS Univ. of Wisconsin, Madison, WI, USA
SO (2003) 112 pp. Avail.: UMI, Order No. DA3101396 From: Diss. Abstr. Int., B 2004, 64(8), 3889
DT Dissertation
LA English
AB Unavailable

L6 ANSWER 15 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:513881 CAPLUS
DN 141:255049
TI Probe design for large-scale molecular biology applications
AU VanBuren, Vincent; Yoshikawa, Toshiyuki; Hamatani, Toshio; Ko, Minoru S. H.
CS National Institute on Aging, Laboratory of Genetics, Developmental Genomics and Aging Section, National Institutes of Health, Baltimore, MD, 21224, USA
SO Proceedings of the IEEE Bioinformatics Conference, 2nd, Stanford, CA, United States, Aug. 11-14, 2003 (2003), Meeting Date 2003, 502-503 Publisher: IEEE Computer Society, Los Alamitos, Calif. CODEN: 69FOVN; ISBN: 0-7695-2000-6
DT Conference
LA English
AB Large-scale mol. biol. technologies such as DNA microarrays and large-scale in situ hybridization (ISH) are used to gain an appreciation of global attributes in biol. tissues and cells. Although many of these efforts use cDNA probes, an approach that makes use of designed oligo probes should offer improved consistency at uniform hybridization conditions and improved specificity, as demonstrated by various oligo microarray platforms. We describe a new Web-based application that takes FASTA-formatted sequences as input, and returns both a list of the best choices for probes and a full report contg. possible alternatives. Probe design for microarrays may use a scoring routine that optimizes probe intensity based upon an artificial neural network (ANN) trained to predict the av. probe intensity from the phys. properties of the probe and a screen for possible cross-reactivity. This new tool should provide a reliable way to construct probes that maximize signal intensity while minimizing cross-reactivity. The Web-based Probe Hunter application is available at http://probeworkshop.grc.nia.nih.gov.
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 16 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:513878 CAPLUS
DN 141:237255
TI Gene selection for multi-class prediction of microarray data
AU Chen, Dechang; Hua, Dong; Reifman, Jaques; Cheng, Xiuzhen
CS Uniformed Services, University of the Health Sciences, Israel
SO Proceedings of the IEEE Bioinformatics Conference, 2nd, Stanford, CA, United States, Aug. 11-14, 2003 (2003), Meeting Date 2003, 492-495 Publisher: IEEE Computer Society, Los Alamitos, Calif. CODEN: 69FOVN; ISBN: 0-7695-2000-6
DT Conference
LA English
AB Gene expression data from microarrays have been successfully applied to class prediction, where the purpose is to classify and predict the diagnostic category of a sample by its gene expression profile. A typical microarray dataset consists of expression levels for a large no. of genes on a relatively small no. of samples. As a consequence, one basic and important question assocd. with class prediction is; how do we identify a small subset of informative genes contributing the most to the classification task. Many methods have been proposed but most focus on two-class problems, such as discrimination between normal and disease samples. This paper addresses selecting informative genes for multi-class prediction problems by jointly considering all the classes simultaneously. Our approach is based on the power of the genes is discriminating among the different classes (e.g., tumor types) and the existing correlation between genes. We formulate the expression levels of a given gene by a one-way anal. of variance model with heterogeneity of variances, and det. the discriminatory power of the gene by a test statistic designed to test the equality of the class means. In other words, the discriminatory power of a gene is assocd. with a Behrens-Fisher problem. Informative genes are chosen such that each selected gene has a high discriminatory power and the correlation between any pair of selected genes is low. Test statistics considered in this paper include the ANOVA F test statistic, the Brown-Forsythe test statistic, the Cochran test statistic, and the Welch test statistic. Their performances are evaluated over several classification methods applied to two publicly available microarray datasets. The results show that Brown-Forsythe test statistic achieves the best performance.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 17 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:513856 CAPLUS
DN 142:218658
TI MageBuilder: a schema translation tool for generating MAGE-ML from tabular microarray data
AU Martin, William; Horton, Robert M.
CS Attotron Biosensor Corporation, USA
SO Proceedings of the IEEE Bioinformatics Conference, 2nd, Stanford, CA, United States, Aug. 11-14, 2003 (2003), Meeting Date 2003, 431-432 Publisher: IEEE Computer Society, Los Alamitos, Calif. CODEN: 69FOVN; ISBN: 0-7695-2000-6
DT Conference
LA English
AB A 'MageBuilder' object takes a set of 'MageMap' objects and a set of data streams as input, and produces a MAGEstk object representation, which is then serialized as MAGE-ML. A 'MageMap' object encapsulates the rules of how data records from an input stream relate to one MAGE object. Each input "stream" is an anonymous subroutine that supplies records whose fields represent columns in the input table. The input tables can be delimited text files, database queries, or essentially any source that can be coerced into a set of records with fixed fields.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 18 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:513855 CAPLUS
DN 141:255419
TI Wavelet transforms for the analysis of microarray experiments
AU Tokuyasu, Taku A.; Albertson, Donna; Pinkel, Dan; Jain, Ajay
CS UCSF Cancer Center, San Francisco, CA, 94143-0128, USA
SO Proceedings of the IEEE Bioinformatics Conference, 2nd, Stanford, CA, United States, Aug. 11-14, 2003 (2003), Meeting Date 2003, 429-430 Publisher: IEEE Computer Society, Los Alamitos, Calif. CODEN: 69FOVN; ISBN: 0-7695-2000-6
DT Conference
LA English
AB Array comparative genomic hybridization (cgh) is a microarray technol. for measuring the relative copy no. of thousands of genomic regions. Visual examn. of cgh profiles shows that genomic changes occur on a variety of length scales. Such changes may be characteristic of phenotypic variables such as tumor type and gene mutational status. To aid in identifying such features and exploring their relationship with phenotypic outcomes, we are applying wavelet transforms to the anal. of such profiles. This allows us to decomp. a cgh signal into components on different length scales, even when the genome is severely aberrated, providing a convenient basis for exploring their behavior. Wavelet transforms may also be useful in the realm of gene expression. The expression signal given by genes in clustered order can be wavelet transformed, which compresses the signal from many genes into a few components, possibly aiding in the development of new tumor classifiers.

RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 19 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:513850 CAPLUS
DN 141:237250
TI A flexible pipeline for experimental design, processing, and analysis of microarray data
AU Osborn, Stephen; Kennedy, Scot; Chin, Daniel
CS PPD Discovery, Inc., Menlo Park, CA, 94025, USA
SO Proceedings of the IEEE Bioinformatics Conference, 2nd, Stanford, CA, United States, Aug. 11-14, 2003 (2003), Meeting Date 2003, 411-412 Publisher: IEEE Computer Society, Los Alamitos, Calif. CODEN: 69FOVN; ISBN: 0-7695-2000-6
DT Conference
LA English
AB We created a web-based microarray data anal. pipeline for managing the vols. of data created by prodn. microarray expts. Expts. are formalized by grouping array data into hierarchies based on types such as "dye swap" or "replicate.". Grouping dets. the anal. to be performed and enables the tool to automatically generate reports and charts appropriate to the expt. results. Subsets of data across arrays may also be hierarchically grouped into types such as "gene" or "list.". The group hierarchy is similar to a document object model (DOM), which enables queries to be posed in an XPath or XQuery language. Analyzer modules provide the complicated statistical processing and may be custom written or implemented as wrappers around existing tools. For speculative data anal. or publication, the results may be exported to a std. format.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 20 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:513814 CAPLUS
DN 141:237619
TI Fourier harmonic approach for visualizing temporal patterns of gene expression data
AU Zhang, Li; Zhang, Aidong; Ramanathan, Murali
CS Department of Computer Science and Engineering, State University of New York at Buffalo, Buffalo, NY, 14260, USA
SO Proceedings of the IEEE Bioinformatics Conference, 2nd, Stanford, CA, United States, Aug. 11-14, 2003 (2003), Meeting Date 2003, 137-147 Publisher: IEEE Computer Society, Los Alamitos, Calif. CODEN: 69FOVN; ISBN: 0-7695-2000-6
DT Conference
LA English
AB DNA microarray technol. provides a broad snapshot of the state of the cell by measuring the expression levels of thousands of genes simultaneously. Visualization techniques can enable the exploration and detection of patterns and relationships in a complex dataset by presenting the data in a graphical format in which the key characteristics become more apparent. The purpose of this study is to present an interactive visualization technique conveying the temporal patterns of gene expression data in a form intuitive for non-specialized end-users. The first Fourier harmonic projection (FFHP) was introduced to translate the multi-dimensional time series data into a two dimensional scatter plot. The spatial relationship of the points reflect the structure of the original dataset and relationships among clusters become two dimensional. The proposed method was tested using two published, array-derived gene expression datasets. These results demonstrate the effectiveness of the approach.
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 21 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:513811 CAPLUS
DN 141:237618
TI Combining microarrays and biological knowledge for estimating gene networks via Bayesian networks
AU Imoto, Seiya; Higuchi, Tomoyuki; Goto, Takao; Tashiro, Kousuke; Kuhara, Satoru; Miyano, Satoru
CS Human Genome Center, Institute of Medical Science, University of Tokyo, Tokyo, 108-8639, Japan
SO Proceedings of the IEEE Bioinformatics Conference, 2nd, Stanford, CA, United States, Aug. 11-14, 2003 (2003), Meeting Date 2003, 104-113 Publisher: IEEE Computer Society, Los Alamitos, Calif. CODEN: 69FOVN; ISBN: 0-7695-2000-6
DT Conference
LA English
AB We propose a statistical method for estg. a gene network based on Bayesian networks from microarray gene expression data together with biol. knowledge including protein-protein interactions, protein-DNA interactions, binding site information, existing literature and so on. Unfortunately, microarray data do not contain enough information for constructing gene networks accurately in many cases. Our method adds biol. knowledge to the estn. method of gene networks under a Bayesian statistical framework, and also controls the trade-off between microarray information and biol. knowledge automatically. We conduct Monte Carlo simulations to show the effectiveness of the proposed method. We analyze Saccharomyces cerevisiae gene expression data as an application.
RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 22 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:513807 CAPLUS
DN 141:237615
TI Fast and accurate probe selection algorithm for large genomes
AU Sung, Wing-Kin; Lee, Wah-Heng
CS Department of Computer Science, National University of Singapore, Singapore, Singapore
SO Proceedings of the IEEE Bioinformatics Conference, 2nd, Stanford, CA, United States, Aug. 11-14, 2003 (2003), Meeting Date 2003, 65-74 Publisher: IEEE Computer Society, Los Alamitos, Calif. CODEN: 69FOVN; ISBN: 0-7695-2000-6
DT Conference
LA English
AB The oligo microarray (DNA chip) technol. in recent years has a significant impact on genomic study. Many fields such as gene discovery, drug discovery, toxicol. research and disease diagnosis, will certainly benefit from its use. A microarray is an orderly arrangement of thousands of DNA fragments where each DNA fragment is a probe (or a fingerprint) of a gene/cDNA. It is important that each probe must uniquely assoc. with a particular gene/cDNA. Otherwise, the performance of the microarray will be affected. Existing algorithms usually select probes using the criteria of homogeneity, sensitivity, and specificity. Moreover, they improve efficiency employing some heuristics. Such approaches reduce the accuracy. Instead, the authors make use of some smart filtering techniques to avoid redundant computation while maintaining the accuracy. Based on the new algorithm, optimal short (20 bases) or long (50 or 70 bases) probes can be computed efficiently for large genomes.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 23 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:513806 CAPLUS
DN 141:237614
TI Fast and sensitive probe selection for DNA chips using jumps in matching statistics
AU Rahmann, Sven
CS Dept. of Computational Molecular Biology, Max Planck Institute for Molecular Genetics, Berlin, D-14195, Germany
SO Proceedings of the IEEE Bioinformatics Conference, 2nd, Stanford, CA, United States, Aug. 11-14, 2003 (2003), Meeting Date 2003, 57-64 Publisher: IEEE Computer Society, Los Alamitos, Calif. CODEN: 69FOVN; ISBN: 0-7695-2000-6
DT Conference
LA English
AB The design of large scale DNA microarrays is a challenging problem. So far, probe selection algorithms must trade the ability to cope with large scale problems for a loss of accuracy in the estn. of probe quality. Tha author presents an approach based on jumps in matching statistics that combines the best of both worlds. This article consists of two parts. The first part is theor. The author introduces the notion of jumps in matching statistics between two strings and derive their properties. The author ests. the frequency of jumps for random strings in a non-uniform Bernoulli model and present a new heuristic argument to find the center of the length distribution of the longest substring that two random strings have in common. The results are generalized to near-perfect matches with a small no. of mismatches. In the second part, the author uses the concept of jumps to improve the accuracy of the longest common factor approach for probe selection by moving from a string-based to an energy-based specificity measure, while only slightly more than doubling the selection time.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 24 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:429171 CAPLUS
DN 141:134846
TI MicroPreP: A cDNA microarray data pre-processing framework
AU Van Hijum, Sacha Aft; De La Nava, Jorge Garcia; Trelles, Oswaldo; Kok, Jan; Kuipers, Oscar P.
CS Molecular Genetics Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, Haren, Neth.
SO Applied Bioinformatics (2003), 2(4), 241-244 CODEN: ABPIC8; ISSN: 1175-5636
PB Open Mind Journals
DT Journal
LA English
AB The user-friendly MicroPreP framework was developed to transform raw intensity data from cDNA microarrays into high-quality data. The main features of this software are: LOWESS normalization; merging of DNA microarray data from changing slide versions; outlier detection; and slide quality assessment. The software is available at http://molgen.biol.rug.nl/molgen/research/molgensoftware.php.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 25 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:378314 CAPLUS
DN 141:83115
TI Genetic algorithms applied to multi-class clustering for gene expression data
AU Pan, Haiyan; Zhu, Jun; Han, Danfu
CS Institute of Bioinformatics, Zhejiang University, Hangzhou, 310029, Peop. Rep. China
SO Genomics, Proteomics & Bioinformatics (2003), 1(4), 279-287 CODEN: GPBEBL; ISSN: 1672-0229
PB Science Press
DT Journal
LA English
AB A hybrid GA (genetic algorithm)-based clustering (HGACLUS) schema, combining merits of the Simulated Annealing, was described for finding an optimal or near-optimal set of methods. This schema maximized the clustering success by achieving internal cluster cohesion and external cluster isolation. The performance of HGACLUS and other methods was compared by using ***simulated*** data and open

microarray gene-expression datasets. HGACLUS was generally found to be more accurate and robust than other methods discussed in this paper by the exact validation strategy and the explicit cluster no.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 26 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:377428 CAPLUS
DN 141:100612
TI Microarray experimental design: power and sample size considerations
AU Yang, M. C. K.; Yang, J. J.; McIndoe, R. A.; She, J. X.
CS Department of Statistics, University of Florida, Gainesville, FL, 32611, USA
SO Physiological Genomics (2003), 16(1), 24-28 CODEN: PHGEFP; ISSN: 1094-8341
URL: http://physiolgenomics.physiology.org/cgi/reprint/16/1/24.pdf
PB American Physiological Society
DT Journal; (online computer file)
LA English
AB Gene expression anal. using high-throughput microarray technol. has become a powerful approach to study systems biol. The exponential growth in microarray expts. has spawned a no. of investigations into the reliability and reproducibility of this type of data. However, the sample size requirements necessary to obtain statistically significant results has not had as much attention. The statistical methods for the detn. of the sufficient no. of subjects necessary to minimize the false discovery rate while maintaining high power to detect differentially expressed genes was reported here. Two exptl. designs were considered: a comparison between two groups at a single time point, and a comparison of two exptl. groups with sequential time points. Computer programs are available for the methods discussed in this paper and are adaptable to more complicated situations.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 27 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:374678 CAPLUS
DN 141:82997
TI Strategies for clustering, classifying, integrating, standardizing and visualizing microarray gene expression data
AU Granda, Willy Valdivia
CS Genomics and Bioinformatics Group, Department of Plant Pathology, North Dakota State University, USA
SO Beginner's Guide to Microarrays (2003), 277-340. Editor(s): Blalock, Eric M. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69FIT3; ISBN: 1-4020-7472-7
DT Conference; General Review
LA English
AB A review aimed at introducing the reader to the basic concepts underlying the statistical and data mining methods used for the anal. of microarray data. An attempt is made to provide an introductory review and a basic guide on microarray data anal. strategies, complex math. equations and their computational implementations. This review does not include early comparative gene expression anal. using microarrays where gene expression was established in terms of fold change. An inherent problem with this criterion is that genes with low abs. expression levels have a greater inherent error in their measurements and are more likely than higher expressing genes to meet any fold change cut-off. Different concepts related to the microarray data anal. process including microarray gene expression matrix, outliers, missing values, distance functions, unsupervised and supervised methods, advantages, limitations and considerations to est. their reliability are presented. When it is necessary, biol. examples are provided with the aim to highlight the relevance of some microarray data anal. methods. This review also introduces information about software (public and private) that can help the reader to choose suitable tools for the anal. of their particular microarray gene expression data. Some aspects about the implementation of microarray data repositories, the development of stds. including the Min. Information About Microarray Expts. (MIAME) and its computational implementation through MAGE-OM, MAGE-ML and MAGE-stk are highlighted. Finally, current trends and future challenges that microarray technol. will present are also summarized.
RE.CNT 149 THERE ARE 149 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 28 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:374670 CAPLUS
DN 141:100486
TI Printing technologies and microarray manufacturing techniques: making the perfect microarray
AU Martinsky, Todd
CS TeleChem International, Sunnyvale, CA, USA
SO Beginner's Guide to Microarrays (2003), 93-122. Editor(s): Blalock, Eric M. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69FIT3; ISBN: 1-4020-7472-7
DT Conference; General Review
LA English
AB A review and discussion of protocols for the prodn. of DNA and protein microarrays with the consistency and accuracy needed for FDA approval as diagnostic and drug testing devices. The regulation of robotics, surface chem., sample prepn. and environment in the prodn. of microarrays is discussed.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 29 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:277170 CAPLUS
DN 142:109824
TI Development of a universal microarray system for the detection of rickettsiae
AU Cui, Hong; Chen, Xiaping; Chen, Meiling; Guo, Zhaobiao; Wang, Jin; Zhai, Junhui; Yang, Ruifu
CS Institute of Microbiology and Epidemiology, Beijing, 100071, Peop. Rep. China
SO Junshi Yixue Kexueyuan Yuankan (2003), 27(3), 186-188, 222 CODEN: JYKYEL; ISSN: 1000-5501
PB Junshi Yixue Kexueyuan Yuankan Bianjibu
DT Journal
LA Chinese
AB A microarray-based detection system was developed, which employs 16S rDNA sequence as its detection target for rapid and efficient detection of rickettsiae. Specific probes targeting 6 species of rickettsiae were designed by using some bioinformatics softwares and methods. Ten strains of Bickettsiae were tested by using this microarray system. The results showed that Bartonella henselae, Orientia tsutsugamushi, Rickettsia rickettsii, R. prowazeki, Coxiella burnetii could be detected at species or genus level. For example, R. rickettsii had a cross reaction with 3 out of 4 probes specifically targeting R.prowazekii, while R.prowazekii hybridized with only 2 R.rickettsii's probes. Ehrlichia canis was neg. throughout the whole expt. and the reason was under evaluation. The sensitivity assay was performed by employing serial diln. of C. burnetii chromosomal DNA. The sensitivity of detection system used was found to be 10 times higher than that of PCR-electrophoresis. The oligonucleotide microarray could det. most of the test strains at species level. The overall time for sample process, hybridization and data acquisition lasts about 4.5 h. The oligonucleotide microarray can be used for the detection of rickettsiae.

L6 ANSWER 30 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:276341 CAPLUS
DN 141:139819
TI Processing and analysis of DNA microarrays
AU Choi, Heejun
CS Univ. of Louisville, Louisville, KY, USA
SO (2003) 179 pp. Avail.: UMI, Order No. DA3089502 From: Diss. Abstr. Int., B 2003, 64(5), 2261
DT Dissertation
LA English
AB Unavailable

L6 ANSWER 31 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:275877 CAPLUS
DN 141:117808
TI Computational methods for transcription analysis using oligonucleotide microarrays
AU Tjaden, Brian Curtis
CS Univ. of Washington, Seattle, WA, USA
SO (2003) 169 pp. Avail.: UMI, Order No. DA3091082 From: Diss. Abstr. Int., B 2003, 64(5), 2273
DT Dissertation
LA English
AB Unavailable

L6 ANSWER 32 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:176863 CAPLUS
DN 140:333078
TI High-throughput functional inference in the post-genomic era
AU Spira, Avrum; Yanai, Itai; Chaterjee, Rakesh; Wu, Jie; Harrison-Tang, Rhonda; DeLisi, Charles
CS Bioinformatics Graduate Program, Division of Pulmonary Medicine, Boston University, Boston, MA, USA
SO Perspectives in Gene Expression (2003), 345-358. Editor(s): Appasani, Krishnarao. Publisher: Eaton Publishing Co., Westborough, Mass. CODEN: 69FDMF; ISBN: 1-881299-16-3
DT Conference; General Review
LA English
AB A review. High-throughput inferential methods such as domain fusion, chromosomal proximity, and phylogenetic profiling and exptl. technologies including high-d. arrays of probes for detecting expressed genes are discussed. The application of microarrays to classification of cancers and cancer pathogenesis as well as to host response to pathogens are also discussed.
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 33 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:130873 CAPLUS
DN 140:265037
TI The emerging utility of oligonucleotide microarrays
AU Kane, Michael D.; Dombkowski, Alan A.; Madore, Steven J.
CS Genomic Research and Development, Genomic Solutions, Ann Arbor, MI, USA
SO Gene Cloning and Expression Technologies (2002), 537-547. Editor(s): Weiner, Michael P.; Lu, Quinn. Publisher: Eaton Publishing Co., Westborough, Mass. CODEN: 69FBF2; ISBN: 1-881299-20-1
DT Conference; General Review
LA English
AB A review discusses the utility of oligo-probe microarrays for expression profiling in comparison with cDNA-probe microarrays. It describes the computational considerations for oligo-probe attachment, the chem. requirements of oligo-probe attachment, labeling methodologies, and the use of oligo-probe arrays for single nucleotide polymorphism detection.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 34 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:123665 CAPLUS
DN 140:247795
TI Examination of a significant data analysis in quantification of gene-expression by DNA-array
AU Niimura, Yukio; Kodama, Mariko; Ohkawa, Tomi
CS Research Center of Biomedical Analysis and Radio-isotope, Teikyo University School of Medicine, Itabashi-ku, Tokyo, 173-8605, Japan
SO Radioisotopes (2003), 52(11), 617-622 CODEN: RAISAB; ISSN: 0033-8303
PB Nippon Aisotopu Kyokai
DT Journal
LA Japanese
AB Obtaining abundant information on the expression of many genes occurring simultaneously in cells by the DNA array anal. technol. is very important in the life science research. However, the data processing method affects the result greatly. In this paper, the program named as EX-ARRAY was prepd. to verify the macro-array data, which was analyzed by 33P labeling probe, and examd. The original data was obtained from the software Array Gauge and was processed by setting two different backgrounds. Two resulting data were exported as text files, and were input to EX-ARRAY. Processing through this program enhanced the reliability on data anal.

L6 ANSWER 35 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:102966 CAPLUS
DN 140:247785
TI Regression approaches for microarray data analysis
AU Segal, Mark R.; Dahlquist, Kam D.; Conklin, Bruce R.
CS Department of Epidemiology and Biostatistics, University of California, San Francisco, CA, 94143-0560, USA
SO Journal of Computational Biology (2003), 10(6), 961-980 CODEN: JCOBEM; ISSN: 1066-5277
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB A variety of new procedures have been devised to handle the two-sample comparison (e.g., tumor vs. normal tissue) of gene expression values as measured with microarrays. Such new methods are required in part because of some defining characteristics of microarray-based studies: (i) the very large no. of genes contributing expression measures which far exceeds the no. of samples (observations) available and (ii) the fact that by virtue of pathway/network relationships, the gene expression measures tend to be highly correlated. These concerns are exacerbated in the regression setting, where the objective is to relate gene expression, simultaneously for multiple genes, to some external outcome or phenotype. Correspondingly, several methods have been recently proposed for addressing these issues. We briefly critique some of these methods prior to a detailed evaluation of gene harvesting. This reveals that gene harvesting, without addnl. constraints, can yield artifactual solns. Results obtained employing such constraints motivate the use of regularized regression procedures such as the lasso, least angle regression, and support vector machines. Model selection and soln. multiplicity issues are also discussed. The methods are evaluated using a microarray-based study of cardiomyopathy in transgenic mice.
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 36 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:102962 CAPLUS
DN 140:247674
TI Linear models for microarray data analysis: Hidden similarities and differences
AU Kerr, M. Kathleen
CS Department of Biostatistics, University of Washington, Seattle, WA, 98195, USA
SO Journal of Computational Biology (2003), 10(6), 891-901 CODEN: JCOBEM; ISSN: 1066-5277
PB Mary Ann Liebert, Inc.
DT Journal; General Review
LA English
AB A review, with refs. In the past several years many linear models have been proposed for analyzing two-color microarray data. As presented in the literature, many of these models appear dramatically different. However, many of these models are reformulations of the same basic approach to analyzing microarray data. This paper demonstrates the equivalence of some of these models. Attention is directed at choices in microarray data anal. that have a larger impact on the results than the choice of linear model.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 37 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:91766 CAPLUS
DN 141:119706
TI DNA microarrays: An imaging study
AU Kim, C.; Li, M.; Lowe, A.; Venkataramalah, N.; Richmond, K.; Kaysen, J.; Cerrina, F.
CS Center for Nanotechnology and ECE Department, University of Wisconsin-Madison, Madison, WI, 53706, USA
SO Journal of Vacuum Science & Technology, B: Microelectronics and Nanometer Structures--Processing, Measurement, and Phenomena (2003), 21(6), 2946-2950 CODEN: JVSTBM; ISSN: 1071-1023
PB American Institute of Physics
DT Journal
LA English
AB DNA chips are used to study the compn. of genetic material. We report the results of an exptl. study of the synthesis of DNA microarrays using a maskless photodeprotection process. In these "chips," the quality of the final product is dependent on the type and frequency of errors in the synthesis of the oligonucleotides. Contrary to photoresist, the photochem. is linear and thus more prone to the introduction of defects. To understand and characterize the exposure process, we have developed a theor. image formation model based on std. lithog. modeling tools. Exptl., we have used a microarray synthesizer similar to that described in (Ref. 1), but using an argon ion laser as radiation source. To characterize the process, we have acquired aerial images using a CCD camera, a photosensitive film, and fluorescence image of a T-base monomer. We will discuss the imaging properties of the optical system, the models used to analyze the data and the relation between measured images and DNA stepwise synthesis yield.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 38 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:89744 CAPLUS
DN 141:327693
TI Bioinformatics approaches to medical imaging and microarray studies
AU Wang, Zuyi
CS Catholic Univ. of America, Washington, DC, USA
SO (2003) 108 pp. Avail.: UMI, Order No. DA3084451 From: Diss. Abstr. Int., B 2003, 64(3), 1362
DT Dissertation
LA English
AB Unavailable

L6 ANSWER 39 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:6728 CAPLUS
DN 140:234099
TI The design of a gene chip for functional immunological studies on a high-quality control platform
AU Waukau, Jill; Jailwala, Parthav; Wang, Youmin; Khoo, Huoy-Jii; Ghosh, Soumitra; Wang, Xujing; Hessner, Martin J.
CS Max McGee National Research Center for Juvenile Diabetes, Department of Pediatrics, Medical College and Children's Hospital of Wisconsin, Milwaukee, WI, 53226, USA
SO Annals of the New York Academy of Sciences (2003), 1005(Immunology of Diabetes II), 284-287 CODEN: ANYAA9; ISSN: 0077-8923
PB New York Academy of Sciences
DT Journal
LA English
AB We have created an immunol.-related microarray chip contg. primarily known genes with well-studied functional properties. By looking at known genes rather than expressed sequence tags, we hope to gain a better understanding of immunol. pathways and how they work. The immunol. gene chip contains genes from the following functional categories: T cell genes; B cell genes; dendritic cell genes; chemokine and cytokine genes; apoptosis genes; cell cycle genes; cell interaction genes; general hematol. and immunol. genes; and adhesion genes. We have also developed a novel three-color cDNA array platform in which arrays are directly visualized before hybridization, which allows us to select only high-quality chips for our expts. In an effort to provide quant. quality control for each array element as well as the entire chip, we have developed Matarray, a software package for image processing and data acquisition. With Matarray, we have built a quant. data filtering and normalization scheme that has proved to be more efficient than the existing methods. The list of immunol. chip genes is available from the authors.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 40 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:990345 CAPLUS
DN 140:158480
TI Quantification of cross hybridization on oligonucleotide microarrays
AU Zhang, Li; Coombes, Kevin R.; Xiao, Lianchun
CS Department of Biostatistics, The University of Texas MD Anderson Cancer Center, Houston, TX, USA
SO Methods of Microarray Data Analysis III, Papers from CAMDA '02, 3rd, Durham, NC, United States, Nov. 14-15, 2002 (2003), Meeting Date 2002, 175-184. Editor(s): Johnson, Kimberly F.; Lin, Simon M. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69EWQ3; ISBN: 1-4020-7582-0
DT Conference
LA English
AB Cross hybridization on microarrays generates signals from unintended genes, which presents a special challenge in gene expression profiling studies since it directly leads to false positives. However, little is known about the extent of cross hybridization and why certain probes are particularly prone to cross hybridization. Recently, we developed a free-energy model of binding interactions on oligonucleotide arrays that can decomp. the obsd. probe signals in terms of the effects of gene-specific and generic non-specific binding. We analyzed the data set provided by Affymetrix Inc., which followed a Latin square design with 14 genes spiked-in at various concns. Around 31 probesets show reproducible response to the spiked-in genes. In most cases, we were able to ext. the amt. of cross hybridization signal and identify the source, i.e., the fragments of spiked-in genes that match the cross hybridizing probes. These findings demonstrate the utility of our model for identifying spurious cross-hybridization signals and obtaining robust measure of gene expression levels.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 41 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:990343 CAPLUS

DN 140:176178
TI How many mice and how many arrays? Replication in mouse cDNA microarray experiments
AU Cui, Xiangqin; Churchill, Gary A.
CS The Jackson Laboratory, Bar Harbor, ME, USA
SO Methods of Microarray Data Analysis III, Papers from CAMDA '02, 3rd, Durham, NC, United States, Nov. 14-15, 2002 (2003), Meeting Date 2002, 139-154. Editor(s): Johnson, Kimberly F.; Lin, Simon M. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69EWQ3; ISBN: 1-4020-7582-0
DT Conference
LA English
AB Biol. and tech. variances were estd. from the Project Normal data using the mixed model anal. of variance. The tech. variance is larger than the biol. variance in most genes. In expts. for detecting treatment effects using a ref. design, increasing the no. of mice per treatment is more effective than pooling mice or increasing the no. of arrays per mouse. For a given no. of arrays, more mice per treatment with fewer arrays per mouse are more powerful than fewer mice per treatment with more arrays per mouse. A formula is provided for computing the optimum no. of arrays per mouse to minimize the total cost of the expt.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 42 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:990342 CAPLUS
DN 140:176177
TI Simultaneous assessment of transcriptomic variability and tissue effects in the normal mouse
AU Deng, Shibing; Chu, Tzu-Ming; Wolfinger, Russ
CS SAS Institute, Cary, NC, USA
SO Methods of Microarray Data Analysis III, Papers from CAMDA '02, 3rd, Durham, NC, United States, Nov. 14-15, 2002 (2003), Meeting Date 2002, 125-137. Editor(s): Johnson, Kimberly F.; Lin, Simon M. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69EWQ3; ISBN: 1-4020-7582-0
DT Conference
LA English
AB We consider two linear mixed models for the normal mouse data [Pritchard et al., 2001]. One models the log2 intensity measurements directly and the other models the log2 ratios. In each approach, we treat a mouse as a fixed effect, and alternatively, we also model it as a random effect to assess its variability directly. We compare the results from these mixed model approaches. The models agree that array variance is much larger than other sources of variability, but differ somewhat in their lists of genes exhibiting the most significant mouse effects. Under a Bonferroni criterion, the ratio-based model we consider produces more genes with significant mouse effects than the intensity-based model, but fewer genes with significant tissue effects. Both models demonstrate a general statistical framework for concurrently estg. sources of variability and assessing their significance.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 43 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:990341 CAPLUS
DN 140:176176
TI Comparison of normalization methods for cDNA microarrays
AU Warren, Liling; Liu, Ben
CS Bio-informatics Group Inc., Cary, NC, 27511, USA
SO Methods of Microarray Data Analysis III, Papers from CAMDA '02, 3rd, Durham, NC, United States, Nov. 14-15, 2002 (2003), Meeting Date 2002, 105-121. Editor(s): Johnson, Kimberly F.; Lin, Simon M. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69EWQ3; ISBN: 1-4020-7582-0
DT Conference
LA English
AB In a study done by Pritchard et al. [2001], normal gene expression variation was examd. in six genetically identical male mice, to det. a baseline variation for gene expression studies in mice. In this paper, we use data from their study to accomplish the following three goals:. 1) Evaluate five data normalization procedures along with two methods omitting data normalization, and study their impact on identifying baseline differentially expressed genes;. 2) Perform pair-wise comparisons using McNemar's tests on five normalization methods and two methods omitting the normalization step;. 3) Address data quality issues and examine the effect of normalization on anal. results for genes that do not meet either or both of the two data quality criteria. Depending on which normalization method is used, whether omitting the normalization step or not, the no. of genes and the set of the genes identified as differentially expressed from the same study can be substantially different. Anal. demonstrates that when data quality is not ensured, performing normalization can add noise to the data and can bias gene-based ANOVA results. Thus we conclude that ensuring data quality and establishing quality control measures is crucial to increase the effectiveness of normalization procedures and the accuracy of data anal. results. The study also reconfirmed that proper exptl. design and establishing rigorous data quality control stds. are indispensable factors for the success of a microarray expt.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 44 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:990339 CAPLUS
DN 140:176174
TI Characterization, modeling, and ***simulation*** of mouse ***microarray*** data
AU Lalush, David S.
CS Bioinformatics Research Center, North Carolina State University, Raleigh, NC, USA
SO Methods of Microarray Data Analysis III, Papers from CAMDA '02, 3rd, Durham, NC, United States, Nov. 14-15, 2002 (2003), Meeting Date 2002, 75-91. Editor(s): Johnson, Kimberly F.; Lin, Simon M. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69EWQ3; ISBN: 1-4020-7582-0
DT Conference
LA English
AB We developed methods for characterizing a set of ***microarray*** images and for subsequently ***simulating*** ***microarray*** images with statistical properties similar to those in the original set. Characterization involved measuring properties of individual spots and performing anal. of variance to det. the relative contributions of individual pins used for printing and individual slides to the variation obsd. in spot phys. properties, slide background properties, and intensity of individual genes. Slide backgrounds and individual spot nonuniformities were modeled as 2D causal Markov random fields, and parameters for these were derived from the set of real images. The results of the characterization were then used to generate realistic replicates of the original dataset that can be used for evaluating microarray data processing and anal. techniques. We demonstrated the process on a set of microarray images derived from a mouse kidney expt. The characterization of these images showed that slides from two of the six mice have significantly different spot properties from the rest. Simulated images from the set are shown to realistically model most properties of the slides, save for large handling defects. We concluded that characterization should be an important part of any ***microarray*** expt. to maintain quality control, and that realistic ***simulations*** of ***microarray*** images can be produced using these methods.
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 45 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:990000 CAPLUS
DN 140:38421
TI Method and use of protein microarray technology and proteomic analysis to determine efficacy of human and xenographic cell, tissue and organ transplant
IN Mathew, Aby J.; Baust, John M.; Vanbuskirk, Robert; Baust, John G.
PA Biolife Solutions, Inc., USA
SO U.S. Pat. Appl. Publ., 22 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2003232396 A1 20031218 US 2003-372579 20030221
PRAI US 2002-358386P P 20020222
AB The present invention is directed to systems and methods for assessing the success of the transplant of a cell, tissue, or organ before and after transplant. Protein array technol. is used to obtain a biomarker pattern for the cell, tissue, or organ that is being considered for transplant or that has been transplanted. Samples for the identification of biomarkers and biomarker patterns are obtained from the cell, tissue or organ itself, or from a body fluid of the donor or recipient. Sample biomarker data are compared to ref. biomarker data obtained from donors, recipients or cells, tissues or organs that have been transplanted. Correlation of a sample biomarker pattern with the ref. biomarker pattern, where transplant outcome for the samples used for the ref. biomarkers is known, permits a suggested treatment detn. A computerized system to identify the condition of transplant before or after implantation is also provided.

L6 ANSWER 46 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:988231 CAPLUS
DN 140:175875
TI Microarrays for genotyping human group A rotavirus by multiplex capture and type-specific primer extension
AU Lovmar, Lovisa; Fock, Caroline; Espinoza, Felix; Bucardo, Filemon; Syvanen, Ann-Christine; Bondeson, Kare
CS Molecular Medicine, Uppsala University, Uppsala, 751 85, Swed.
SO Journal of Clinical Microbiology (2003), 41(11), 5153-5158 CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB Human group A rotavirus (HRV) is the major cause of severe gastroenteritis in infants worldwide. HRV shares the feature of a high degree of genetic diversity with many other RNA viruses, and therefore, genotyping of this organism is more complicated than genotyping of more stable DNA viruses. We describe a novel microarray-based method that allows high-throughput genotyping of RNA viruses with a high degree of polymorphism by multiplex capture and type-specific extension on microarrays. Denatured reverse transcription (RT)-PCR products derived from two outer capsid genes of clin. isolates of HRV were hybridized to immobilized capture oligonucleotides representing the most commonly occurring P and G genotypes on a microarray. Specific primer extension of the type-specific capture oligonucleotides was applied to incorporate the fluorescent nucleotide analog cyanine 5-labeled dUTP as a detectable label. Laser scanning and fluorescence detection of the ***microarrays*** was followed by visual or ***computer*** -assisted interpretation of the fluorescence patterns generated on the ***microarrays*** . Initially, the method detected HRV in all 40 samples and correctly detd. both the G and the P genotypes of 35 of the 40 strains analyzed. After modification by inclusion of addnl. capture oligonucleotides specific for the initially unassigned genotypes, all genotypes could be correctly defined. The results of genotyping with the microarray fully agreed with the results obtained by nucleotide sequence anal. and sequence-specific multiplex RT-PCR. Owing to its robustness, simplicity, and general utility, the microarray-based method may gain wide applicability for the genotyping of microorganisms, including highly variable RNA and DNA viruses.

RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 47 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:985301 CAPLUS
DN 140:194273
TI Continuous-Time Identification of Gene Expression Models
AU Zak, Daniel E.; Pearson, Ronald K.; Vadigepalli, Rajanikanth; Gonye, Gregory E.; Schwaber, James S.; Doyle, Francis J., III
CS Department of Chemical Engineering, University of Delaware, Newark, DE, USA
SO OMICS (2003), 7(4), 373-386 CODEN: OMICAE; ISSN: 1536-2310
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB One objective of systems biol. is to create predictive, quant. models of the transcriptional regulation networks that govern numerous cellular processes. Gene expression measurements, as provided by microarrays, are commonly used in studies that attempt to infer the regulation underlying these processes. At present, most gene expression models that have been derived from microarray data are based in discrete-time, which have limited applicability to common biol. data sets, and may impede the integration of gene expression models with other models of biol. processes that are formulated as ordinary differential equations (ODEs). To overcome these difficulties, a continuous-time approach for process identification to identify gene expression models based in ODEs was developed. The approach utilizes the modulating functions method of parameter identification. The method was applied to three simulated systems: (1) a linear gene expression model, (2) an autoregulatory gene expression model, and (3) ***simulated*** ***microarray*** data from a nonlinear transcriptional network. In general, the approach was well suited for identifying models of gene expression dynamics, capable of accurately identifying parameters for small nos. of data samples in the presence of modest exptl. noise. Addnl., numerous insights about gene expression modeling were revealed by the case studies.
RE.CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 48 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:982860 CAPLUS
DN 140:158133
TI Oligo design: A ***computer*** program for development of probes for oligonucleotide ***microarrays***
AU Herold, Keith E.; Rasooly, Avraham
CS University of Maryland, College Park, MD, USA
SO BioTechniques (2003), 35(6), 1216-1218,1220-1221 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
AB Oligonucleotide microarrays have demonstrated potential for the anal. of gene expression, genotyping, and mutational anal. Our work focuses primarily on the detection and identification of bacteria based on known short sequences of DNA. Oligo Design, the software described here, automates several design aspects that enable the improved selection of oligonucleotides for use with microarrays for these applications. Two major features of the program are: first, a tiling algorithm for the design of short overlapping temp.-matched oligonucleotides of variable length, which are useful for the anal. of single nucleotide polymorphisms. Second, a set of tools for the anal. of multiple alignments of gene families and related short DNA sequences, which allow for the identification of conserved DNA sequences for PCR primer selection and variable DNA sequences for the selection of unique probes for identification. Note that the program does not address the full genome perspective but, instead, is focused on the genetic anal. of short segments of DNA. The program is Internet-enabled and includes a built-in browser and the automated ability to download sequences from GenBank by specifying the GI no. The program also includes several utilities, including audio recital of a DNA sequence (useful for verifying sequences against a written document), a random sequence generator that provides insight into the relationship between melting temp. and GC content, and a PCR calculator.
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 49 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:980126 CAPLUS
DN 140:193974
TI A CART-based approach to discover emerging patterns in microarray data
AU Boulesteix, Anne-Laure; Tutz, Gerhard; Strimmer, Korbinian
CS Department of Statistics, Seminar for Applied Stochastics, University of Munich, Munich, D-80799, Germany
SO Bioinformatics (2003), 19(18), 2465-2472 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Cancer diagnosis using gene expression profiles requires supervised learning and gene selection methods. Of the many suggested approaches, the method of emerging patterns (EPs) has the particular advantage of explicitly modeling interactions among genes, which improves classification accuracy. However, finding useful (i.e. short and statistically significant) EP is typically very hard. Here we introduce a CART-based approach to discover EPs in microarray data. The method is based on growing decision trees from which the EPs are extd. This approach combines pattern search with a statistical procedure based on Fisher's exact test to assess the significance of each EP. Subsequently, sample classification based on the inferred EPs is performed using max.-likelihood linear discriminant anal. Using simulated data as well as gene expression data from colon and leukemia cancer expts. we assessed the performance of our pattern search algorithm and classification procedure. In the simulations, our method recovers a large proportion of known EPs while for real data it is comparable in classification accuracy with three top-performing alternative classification algorithms. In addn., it assigns statistical significance to the inferred EPs and allows to rank the patterns while simultaneously avoiding overfit of the data. The new approach therefore provides a versatile and computationally fast tool for elucidating local gene interactions as well as for classification.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 50 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:980122 CAPLUS
DN 140:193971
TI Machaon CVE: cluster validation for gene expression data
AU Bolshakova, Nadia; Azuaje, Francisco
CS Department of Computer Science, Trinity College Dublin, Dublin, Ire.
SO Bioinformatics (2003), 19(18), 2494-2495 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB His paper presents a cluster validation tool for gene expression data. Machaon CVE (Clustering and Validation Environment) system aims to partition samples or genes into groups characterized by similar expression patterns, and to evaluate the quality of the clusters obtained.
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 51 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:980094 CAPLUS
DN 140:110790
TI MetaGeneAlyse: analysis of integrated transcriptional and metabolite data
AU Daub, Carsten O.; Kloska, Sebastian; Selbig, Joachim
CS Max Planck Institute of Molecular Plant Physiology, Golm, 14476, Germany
SO Bioinformatics (2003), 19(17), 2332-2333 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Summary: New techniques in sample prepn. allow high throughput anal. of samples on the transcriptional as well as on the metabolic level. We present a service accessible via the web that allows the anal. of integrated data sets that combine gene-expression data and metabolic data. After uploading, data sets can be normalized, clustered by various methods and results can be graphically visualized. All calcns. are carried out on a server, so even time- and memory-consuming analyses can be done independently of the performance of the client.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 52 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:980087 CAPLUS
DN 140:140592
TI Sensitivity and specificity of inferring genetic regulatory interactions from microarray experiments with dynamic Bayesian networks
AU Husmeier, Dirk
CS JCMB, Biomathematics and Statistics Scotland (BioSS), Edinburgh, EH9 3JZ, UK
SO Bioinformatics (2003), 19(17), 2271-2282 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Bayesian networks have been applied to infer genetic regulatory interactions from microarray gene expression data. This inference problem is particularly hard in that interactions between hundreds of genes have to be learned from very small data sets, typically contg. only a few dozen time points during a cell cycle. Most previous studies have assessed the inference results on real gene expression data by comparing predicted genetic regulatory interactions with those known from the biol. literature. This approach is controversial due to the absence of known gold stds., which renders the estn. of the sensitivity and specificity, i.e., the true and (complementary) false detection rate, unreliable and difficult. The objective of the present study is to test the viability of the Bayesian network paradigm in a realistic simulation study. First, gene expression data are simulated from a realistic biol. network involving DNAs, mRNAs, inactive protein monomers and active protein dimers. Then, interaction networks are inferred from these data in a reverse engineering approach, using Bayesian networks and Bayesian learning with Markov chain Monte Carlo. Results: The simulation results are presented as receiver operator characteristics curves. This allows estg. the proportion of spurious gene interactions incurred for a specified target proportion of recovered true interactions. The findings demonstrate how the network inference performance varies with the training set size, the degree of inadequacy of prior assumptions, the exptl. sampling strategy and the inclusion of further, sequence-based information.
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 53 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:980085 CAPLUS
DN 140:123340
TI Normality of oligonucleotide microarray data and implications for parametric statistical analyses
AU Giles, Peter J.; Kipling, David
CS Department of Pathology, University of Wales College of Medicine, Cardiff, CF14 4XN, UK

SO Bioinformatics (2003), 19(17), 2254-2262 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Exptl. limitations have resulted in the popularity of parametric statistical tests as a method for identifying differentially regulated genes in microarray data sets. However, these tests assume that the data follow a normal distribution. To date, the assumption that replicate expression values for any gene are normally distributed, has not been critically addressed for Affymetrix GeneChip data. The normality of the expression values calcd. using four different com. and academic software packages was investigated using a data set consisting of the same target RNA applied to 59 human Affymetrix U95A GeneChips using a combination of statistical tests and visualization techniques. For the majority of probe sets obtained from each anal. suite, the expression data showed a good correlation with normality. The exception was a large no. of low-expressed genes in the data set produced using Affymetrix Microarray Suite 5.0, which showed a striking non-normal distribution. In summary, our data provide strong support for the application of parametric tests to GeneChip data sets without the need for data transformation.
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 54 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:980072 CAPLUS
DN 140:123338
TI MGraph: graphical models for microarray data analysis
AU Wang, Junbai; Myklebost, Ola; Hovig, Eivind
CS Tumor Biology Department, The Norwegian Radium Hospital, Oslo, 0310, Norway
SO Bioinformatics (2003), 19(17), 2210-2211 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB This paper introduces a MATLAB toolbox, MGraph, which applies graphical models as a natural environment to formulate and solve problems in microarray data anal. MGraph with its graphical interface allows the user to predict genetic regulatory networks by a graphical gaussian model (GGM), and to quantify the effects of different exptl. treatment conditions on gene expression profiles by a graphical log-linear model (GLM). The power of graphical models was explored and illustrated through two example applications. First, four MAPK pathways in yeast were meaningfully reconstructed through GGM. Second, GLM was used to quantify the contributions of sex, genotype and age to transcriptional variance in Drosophila melanogaster. This application may provide a valuable aid in the prediction of genetic regulatory networks, as well as in investigations of various exptl. conditions that affect global gene expression profiles. Availability: The MATLAB program MGraph is freely available at for academics at http://www.uio.no/~junbaiw/mgraph/mgraph.htm l.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 55 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:967521 CAPLUS
DN 140:281940
TI Microarray analysis using bioinformatics analysis audit trails (BAATs)
AU Bellgard, Matthew; Hunter, Adam; Kenworthy, William
CS Centre for Bioinformatics and Biological Computing, Murdoch University, Perth, 6150, Australia
SO Comptes Rendus Biologies (2003), 326(10-11), 1083-1087 CODEN: CRBOCM; ISSN: 1631-0691
PB Editions Scientifiques et Medicales Elsevier
DT Journal
LA English
AB Bioinformatics anal. plays an integrative role in genomics and functional genomics. The ability to conduct quality managed, hypothesis-driven bioinformatics anal. with the plethora of data available is mandatory. Biol. interpretation of this data is dependent on versions of databases, programs and the parameters used. Thus, tracking and auditing the analyses process is important. This paper outlines what we term Bioinformatics Anal. Audit Trails (BAATs) and describes YABI, a bioinformatics environment that implements BAATs. YABI can incorporate most bioinformatics tools within the same environment, making it a valuable resource.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 56 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:966343 CAPLUS
DN 140:158117
TI ***Microarray*** data ***simulator*** for improved selection of differentially expressed genes
AU Singhal, Sunil; Kyvernitis, Chris G.; Johnson, Steven W.; Kaiser, Larry R.; Liebman, Michael N.; Albelda, Steven M.
CS Section of Thoracic Surgery, Division of Cardiothoracic Surgery, University of Pennsylvania School of Medicine, Philadelphia, PA, USA
SO Cancer Biology & Therapy (2003), 2(4), 383-391 CODEN: CBTAAO; ISSN: 1538-4047
PB Landes Bioscience
DT Journal
LA English
AB The development of microarray technol. has allowed researchers to measure expression levels of thousands of genes simultaneously. Anal. of these data requires the best normalization and statistical approaches to account for the biol. and tech. variability inherent in the technique. To approach this problem we have developed a publicly available ***simulator*** of ***microarray*** hybridization expts. that can be used to help assess the accuracy of bioinformatic tools in discovering significant genes. After analyzing microarray hybridization expts. from over 50 samples, an est. of various degrees of tech. and biol. variability was obtained. This information was used to develop a ***simulator*** of ***microarray*** hybridization data which modeled "normal-tissue samples" and "diseased tissue samples" with known, defined, changes in gene expression (a "gold std."). The data derived from the simulator were then used to evaluate the true pos. and false neg. rates of several normalization procedures and gene selection techniques. We found that the type of normalization approach used was an important aspect of data anal. Global normalization was the least accurate approach. Evaluation of gene selection techniques showed that "Significance anal. of microarrays" (SAM) and "Patterns of Gene Expression" (PaGE) were more accurate than simple t-test anal. We provide access to the ***microarray*** hybridization ***simulator*** as a public resource for biologists to further test new emerging genomic bioinformatic tools.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 57 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:956046 CAPLUS
DN 140:124659
TI Quantitative microscopic techniques for monitoring dynamic processes in microarrays
AU Van Den Doel, Lennert Richard
CS Technische Universiteit Delft, Delft, Neth.
SO (2002) 156 pp. Avail.: From degree-granting institution From: Diss. Abstr. Int., C 2002, 63(2), 297
DT Dissertation
LA English
AB Unavailable

L6 ANSWER 58 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:955143 CAPLUS
DN 140:122963
TI Global analysis of ligand sensitivity of estrogen inducible and suppressible genes in MCF7/BUS breast cancer cells by DNA microarray
AU Coser, Kathryn R.; Chesnes, Jessica; Hur, Jingyung; Ray, Sandip; Isselbacher, Kurt J.; Shioda, Toshi
CS Department of Tumor Biology and DNA Microarray Core Facility, Massachusetts General Hospital Cancer Center, Charlestown, MA, 02129, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2003), 100(24), 13994-13999 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB To obtain comprehensive information on 17.beta.-estradiol (E2) sensitivity of genes that are inducible or suppressible by this hormone, we designed a method that dets. ligand sensitivities of large nos. of genes by using DNA ***microarray*** and a set of simple Perl ***computer*** scripts implementing the std. metric statistics. We used it to characterize effects of low (0-100 pM) concns. of E2 on the transcription profile of MCF7/BUS human breast cancer cells, whose E2 dose-dependent growth curve satd. with 100 pM E2. Evaluation of changes in mRNA expression for all genes covered by the DNA microarray indicated that, at a very low concn. (10 pM), E2 suppressed .apprxeq.3-5 times larger nos. of genes than it induced, whereas at higher concns. (30-100 pM) it induced .apprxeq.1.5-2 times more genes than it suppressed. Using clearly defined statistical criteria, E2-inducible genes were categorized into several classes based on their E2 sensitivities. This approach of hormone sensitivity anal. revealed that expression of two previously reported E2-inducible autocrine growth factors, transforming growth factor .alpha. and stromal cell-derived factor 1, was not affected by 100 pM and lower concns. of E2 but strongly enhanced by 10 nM E2, which was far higher than the concn. that satd. the E2 dose-dependent growth curve of MCF7/BUS cells. These observations suggested that biol. actions of E2 are derived from expression of multiple genes whose E2 sensitivities differ significantly and, hence, depend on the E2 concn., esp. when it is lower than the satg. level, emphasizing the importance of characterizing the ligand dose-dependent aspects of E2 actions.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 59 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:951300 CAPLUS
DN 140:1564
TI Standardization of DNA microarray data analysis by normalization with plural spike control genes and statistical analysis
IN Ando, Satoshi; Inaba, Niro; Ito, Atsushi; Ito, Satoru; Terasaki, Hiroshi
PA Japan Genome Solutions, Inc., Japan
SO PCT Int. Appl., 147 pp. CODEN: PIXXD2
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2003100422 A1 20031204 WO 2003-JP6677 20030528 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG AU 2003241832 A1 20031212 AU 2003-241832 20030528

PRAI JP 2002-154773 A 20020528 WO 2003-JP6677 W 20030528
AB A method, app., and computer programs are disclosed for analyzing and comparing data obtained from DNA microarray expts. Hybridization, normalization, and various statistical anal. steps such as Euclidean distance, regression correction, are used. Use of multiple control genes as spike-in RNAs, specifically, Renilla luciferase gene, baculovirus gp64 gene, and .lambda. phage ea22 gene, and housekeeping genes, is claimed.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 60 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:940843 CAPLUS
DN 140:175838
TI EMMA: a platform for consistent storage and efficient analysis of microarray data
AU Dondrup, Michael; Goesmann, Alexander; Bartels, Daniela; Kalinowski, Jorn; Krause, Lutz; Linke, Burkhard; Rupp, Oliver; Sczyrba, Alexander; Puhler, Alfred; Meyer, Folker
CS Center for Genome Research, Bielefeld University, Bielefeld, D-33594, Germany
SO Journal of Biotechnology (2003), 106(2-3), 135-146 CODEN: JBITD4; ISSN: 0168-1656
PB Elsevier Science B.V.
DT Journal
LA English
AB As a high throughput technique, microarray expts. produce large data sets, consisting of measured data, lab. protocols, and exptl. settings. We have implemented the open source platform EMMA to store and analyze these data. The system provides automated pipelines for data processing and has a modular architecture that can be easily extended. EMMA features detailed reports about spots and their corresponding measurements. In addn. to routine data anal. algorithms, the system can be integrated with other components that contain addnl. data sources (e.g. genome annotation systems).
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 61 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:938798 CAPLUS
DN 140:158093
TI Improved detection of differentially expressed genes in microarray experiments through multiple scanning and image integration
AU Romualdi, Chiara; Trevisan, Silvia; Celegato, Barbara; Costa, Germano; Lanfranchi, Gerolamo
CS CRIBI Biotechnology Centre and Dipartimento di Biologia, Universita degli Studi di Padova, Padua, 35121, Italy
SO Nucleic Acids Research (2003), 31(23), e149/1-e149/8 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The variability of results in microarray technol. is in part due to the fact that independent scans of a single hybridized microarray give spot images that are not quite the same. To solve this problem and turn it to our advantage, we introduced the approach of multiple scanning and of image integration of microarrays. To this end, we have developed specific software that creates a virtual image that statistically summarizes a series of consecutive scans of a microarray. We provide evidence that the use of multiple imaging (i) enhances the detection of differentially expressed genes; (ii) increases the image homogeneity; and (iii) reveals false-pos. results such as differentially expressed genes that are detected by a single scan but not confirmed by successive scanning replicates. The increase in the final no. of differentially expressed genes detected in a microarray expt. with this approach is remarkable; 50% more for microarrays hybridized with targets labeled by reverse transcriptase, and 200% more for microarrays developed with the tyramide signal amplification (TSA) technique. The results have been confirmed by semi-quant. RT-PCR tests.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 62 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:923139 CAPLUS
DN 140:123215
TI Inferring gene networks from time series microarray data using dynamic Bayesian networks
AU Kim, Sun Yong; Imoto, Seiya; Miyano, Satoru
CS Human Genome Centre, Institute of Medical Science, University of Tokyo, Minato-ku, Tokyo, 108-8639, Japan
SO Briefings in Bioinformatics (2003), 4(3), 228-235 CODEN: BBIMFX; ISSN: 1467-5463
PB Henry Stewart Publications
DT Journal; General Review
LA English
AB A review. Dynamic Bayesian networks (DBNs) are considered as a promising model for inferring gene networks from time series microarray data. DBNs have overtaken Bayesian networks (BNs) as DBNs can construct cyclic regulations using time delay information. In this paper, a general framework for DBN modeling is outlined. Both discrete and continuous DBN models are constructed systematically and criteria for learning network structures are introduced from a Bayesian statistical viewpoint. This paper reviews the applications of DBNs over the past years. Real data applications for Saccharomyces cerevisiae time series gene expression data are also shown.
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 63 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:917091 CAPLUS
DN 140:54128
TI Robust singular value decomposition analysis of microarray data
AU Liu, Li; Hawkins, Douglas M.; Ghosh, Sujoy; Young, S. Stanley
CS National Institute of Statistical Sciences, Research Triangle Park, NC, 27709-4006, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2003), 100(23), 13167-13172 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB In microarray data there are a no. of biol. samples, each assessed for the level of gene expression for a typically large no. of genes. There is a need to examine these data with statistical techniques to help discern possible patterns in the data. The technique applies a combination of math. and statistical methods to progressively take the data set apart so that different aspects can be examd. for both general patterns and very specific effects. Unfortunately, these data tables are often corrupted with extreme values (outliers), missing values, and non-normal distributions that preclude std. anal. The authors develop a robust anal. method to address these problems. The benefits of this robust anal. will be both the understanding of large-scale shifts in gene effects and the isolation of particular sample-by-gene effects that might be either unusual interactions or the result of exptl. flaws. The method requires a single pass and does not resort to complex "cleaning" or imputation of the data table before anal. The authors illustrate the method with a com. data set.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 64 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:916969 CAPLUS
DN 140:109695
TI Identification of repertoires of surface antigens on leukemias using an antibody microarray
AU Belov, Larissa; Huang, Pauline; Barber, Nicole; Mulligan, Stephen P.; Christopherson, Richard I.
CS School Molecular and Microbial Biosciences, University of Sydney, Sydney, Australia
SO Proteomics (2003), 3(11), 2147-2154 CODEN: PROTC7; ISSN: 1615-9853
PB Wiley-VCH Verlag GmbH & Co. KGaA
DT Journal
LA English
AB The authors have previously described a microarray of cluster of differentiation (CD) antibodies that enables concurrent detn. of more than 60 CD antigens on leukocytes. This procedure does not require protein purifn. or labeling, or a secondary detection system. Whole cells are captured by a microarray of 10 nL antibody dots immobilized on a nitrocellulose film on a microscope slide. Distinct patterns of cell binding are obsd. for different leukemias or lymphomas. These hematol. malignancies arise from precursor cells of T- or B-lymphocytic, or myeloid lineages of hematopoiesis. The dot patterns obtained from patients are distinct from those of peripheral blood leukocytes from normal subjects. This microarray technol. has recently undergone a no. of refinements. The microarray now contains more CD antibodies, and a scanner for imaging dot patterns and software for data anal. provide an extensive immunophenotype sufficient for diagnosis of common leukemias. The technol. is being evaluated for diagnosis of leukemias with parallel use of conventional diagnostic criteria.
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 65 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:912730 CAPLUS
DN 139:359876
TI Methods for statistical analysis of mRNA profiles obtained using microarrays
IN Liebovitch, Larry S.; Jirsa, Viktor K.; Shehadeh, Lina A.
PA USA
SO U.S. Pat. Appl. Publ., 19 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2003215866 A1 20031120 US 2003-427294 20030501
PRAI US 2002-376963P P 20020501
AB Models of different patterns of genetic interactions were formulated and used in methods to det. the architecture of genetic interactions from mRNA expression levels measured in microarray expts. The methods can be used to screen biol. systems to identify which systems are candidates for therapeutic intervention. Also provided are machine readable storage and systems for using the disclosed models and methods.

L6 ANSWER 66 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:912713 CAPLUS
DN 139:361250
TI Method and system for normalization of micro array data based on local normalization of rank-ordered, globally normalized data
IN Wolber, Paul K.; Shannon, Karen W.; Fulmer-Smentek, Stephanie B.; Troup, Charles D.; Amorese, Douglas A.; Sampas, Nicholas M.; Ghosh, Srinka; Connell, Scott D.
PA USA
SO U.S. Pat. Appl. Publ., 38 pp. CODEN: USXXCO
DT Patent
LA English

FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2003215807 A1 20031120 US 2002-143547 20020509
PRAI US 2002-143547 20020509
AB A method and system for normalizing two or more mol. array data sets. Input mol. array data sets are sep. globally normalized by, for example, dividing the feature-signal magnitudes of each data set by the geometric mean of the feature-signal magnitudes of the data set. The globally normalized feature signal magnitudes within each data set are ranked in ascending order. A numeric function is created that relates feature-signal magnitudes of the data sets. Only a subset of the features, obtained by selecting features that are similarly ranked in the sep. feature-signal-magnitude rankings for the data sets, is used to construct the numeric function. The numeric function is smoothed by one of many possible different smoothing procedures. The smoothed numeric function is used to rescale the feature-signal magnitude in one data set to the feature-signal magnitude of another data set, or to normalize the data sets to one another by distributing correction terms amongst the feature-signal magnitudes for a feature in each data set.

L6 ANSWER 67 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:901601 CAPLUS
DN 140:252795
TI A design and statistical perspective on microarray gene expression studies in nutrition: the need for playful creativity and scientific hard-mindedness
AU Page, Grier P.; Edwards, Jode W.; Barnes, Stephen; Weindruch, Richard; Allison, David B.
CS Department of Biostatistics, Section on Statistical Genetics, University of Alabama at Birmingham, Birmingham, AL, 35294-0022, USA
SO Nutrition (New York, NY, United States) (2003), 19(11/12), 997-1000 CODEN: NUTRER; ISSN: 0899-9007
PB Elsevier Science Inc.
DT Journal; General Review
LA English
AB A review. The authors' purpose is to highlight some of the past and potential future uses of microarray in nutrition research, while also commenting on some aspects of the design conduct and anal. of microarray data that will leave to improved data quality. In this review article the authors outline some of the aspects of microarray experimentation that must be considered before and during these expts. These topics include: identification of the expt.'s objective (hypothesis), the exptl. design, sample size, statistical anal., data verification, data handling, and exptl. interpretation. In order to illustrate the principles the authors outline in this article the authors use the methods to layout the design of a microarray expt. to study one aspect of the observation that a diet high in soy is assocd. with lower rates of breast cancer. Microarrays are a very powerful tool for studying virtually every nutrition-related disease and trait and can provide valuable insights that are not obtainable with other techniques. However, unless nutrition researchers conduct their studies with scientific hard-mindedness, the studies will be of lower power at least if not completely misleading.
RE.CNT 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 68 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:888924 CAPLUS
DN 140:71738
TI Probabilistic estimation of micro-array data reliability and underlying gene expression
AU Bilke, Sven; Breslin, Thomas; Sigvardsson, Mikael
CS Complex Systems Division, Department of Theoretical Physics, University Of Lund, Lund, SE-223 62, Swed.
SO BMC Bioinformatics (2003), 4, No pp. given CODEN: BBMIC4; ISSN: 1471-2105
URL: http://www.biomedcentral.com/1471-2105/4/40
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB The availability of high throughput methods for measurement of mRNA concns. makes the reliability of conclusions drawn from the data and global quality control of samples and hybridization important issues. We address these issues by an information theoretic approach, applied to discretized expression values in replicated gene expression data. The approach yields a quant. measure of two important parameter classes: First, the probability P(.sigma.|S) that a gene is in the biol. state .sigma. in a certain variety, given its obsd. expression S in the samples of that variety. Second, sample specific error probabilities which serve as consistency indicators of the measured samples of each variety. The method and its limitations are tested on gene expression data for developing murine B-cells and a t-test is used as ref. On a set of known genes it performs better than the t-test despite the crude discretization into only two expression levels. The consistency indicators, i.e. the error probabilities, correlate well with variations in the biol. material and thus prove efficient. The proposed method is effective in detg. differential gene expression and sample reliability in replicated microarray data. Already at two discrete expression levels in each sample, it gives a good explanation of the data and is comparable to std. techniques.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 69 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:886765 CAPLUS
DN 140:105978
TI Sex genes for genomic analysis in human brain: internal controls for comparison of probe level data extraction
AU Galfalvy, Hanga C.; Erraji-Benchekroun, Loubna; Smyrniotopoulos, Peggy; Pavlidis, Paul; Ellis, Steven P.; Mann, J. John; Sibille, Etienne; Arango, Victoria
CS Department of Neuroscience, New York State Psychiatric Institute, New York, NY, 10032, USA
SO BMC Bioinformatics (2003), 4, No pp. given CODEN: BBMIC4; ISSN: 1471-2105
URL: http://www.biomedcentral.com/1471-2105/4/37
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Genomic studies of complex tissues pose unique anal. challenges for assessment of data quality, performance of statistical methods used for data extn., and detection of differentially expressed genes. Ideally, to assess the accuracy of gene expression anal. methods, one needs a set of genes which are known to be differentially expressed in the samples and which can be used as a "gold std.". The authors introduce the idea of using sex-chromosome genes as an alternative to spiked-in control genes or ***simulations*** for assessment of ***microarray*** data and anal. methods. Expression of sex-chromosome genes were used as true internal biol. controls to compare alternate probe-level data extn. algorithms (Microarray Suite 5.0 [MAS5.0], Model Based Expression Index [MBEI] and Robust Multi-array Av. [RMA]), to assess microarray data quality and to establish some statistical guidelines for analyzing large-scale gene expression. These approaches were implemented on a large new dataset of human brain samples. RMA-generated gene expression values were markedly less variable and more reliable than MAS5.0 and MBEI-derived values. A statistical technique controlling the false discovery rate was applied to adjust for multiple testing, as an alternative to the Bonferroni method, and showed no evidence of false neg. results. Fourteen probe sets, representing nine Y- and two X-chromosome linked genes, displayed significant sex differences in brain prefrontal cortex gene expression. In this study, the authors have demonstrated the use of sex genes as true biol. internal controls for genomic anal. of complex tissues, and suggested anal. guidelines for testing alternate oligonucleotide microarray data extn. protocols and for adjusting multiple statistical anal. of differentially expressed genes. The results also provided evidence for sex differences in gene expression in the brain prefrontal cortex, supporting the notion of a putative direct role of sex-chromosome genes in differentiation and maintenance of sexual dimorphism of the central nervous system. Importantly, these anal. approaches are applicable to all microarray studies that include male and female human or animal subjects.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 70 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:886758 CAPLUS
DN 140:71735
TI Cluster stability scores for microarray data in cancer studies
AU Smolkin, Mark; Ghosh, Debashis
CS Department of Healthy Evaluation Sciences, University of Virginia Medical Center, Charlottesville, VA, USA
SO BMC Bioinformatics (2003), 4, No pp. given CODEN: BBMIC4; ISSN: 1471-2105
URL: http://www.biomedcentral.com/1471-2105/4/36
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB A potential benefit of profiling of tissue samples using microarrays is the generation of mol. fingerprints that will define subtypes of disease. Hierarchical clustering has been the primary anal. tool used to define disease subtypes from microarray expts. in cancer settings. Assessing cluster reliability poses a major complication in analyzing output from clustering procedures. While most work has focused on estg. the no. of clusters in a dataset, the question of stability of individual-level clusters has not been addressed. We address this problem by developing cluster stability scores using subsampling techniques. These scores exploit the redundancy in biol. discriminatory information on the chip. Our approach is generic and can be used with any clustering method. We propose procedures for calcg. cluster stability scores for situations involving both known and unknown nos. of clusters. We also develop cluster-size adjusted stability scores. The method is illustrated by application to data three cancer studies; one involving childhood cancers, the second involving B-cell lymphoma, and the final is from a malignant melanoma study. Code implementing the proposed analytic method can be obtained at the second author's website.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 71 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:886752 CAPLUS
DN 140:71732
TI Evaluation of normalization methods for microarray data
AU Park, Taesung; Yi, Sung-Gon; Kang, Sung-Hyun; Lee, Seung Yeoun; Lee, Yong-Sung; Simon, Richard
CS Department of Statistics, Seoul National University, Seoul, S. Korea
SO BMC Bioinformatics (2003), 4, No pp. given CODEN: BBMIC4; ISSN: 1471-2105
URL: http://www.biomedcentral.com/1471-2105/4/33
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Microarray technol. allows the monitoring of expression levels for thousands of genes simultaneously. This novel technique helps us to understand gene regulation as well as gene by gene interactions more systematically. In the microarray expt., however, many undesirable systematic variations are obsd. Even in replicated expt., some variations are commonly obsd. Normalization is the process of removing some sources of variation which affect the measured gene expression levels. Although a no. of normalization methods have been proposed, it has been difficult to decide which methods perform best. Normalization plays an important role in the earlier stage of microarray data anal. The subsequent anal. results are highly dependent on normalization. In this paper, we use the variability among the replicated slides to

compare performance of normalization methods. We also compare normalization methods with regard to bias and mean square error using simulated data. Our results show that intensity-dependent normalization often performs better than global normalization methods, and that linear and nonlinear normalization methods perform similarly. These conclusions are based on anal. of 36 cDNA microarrays of 3,840 genes obtained in an expt. to search for changes in gene expression profiles during neuronal differentiation of cortical stem cells. Simulation studies confirm our findings.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 72 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:885637 CAPLUS
DN 140:74881
TI Differentiation of lobular versus ductal breast carcinomas by expression microarray analysis
AU Korkola, James E.; DeVries, Sandy; Fridlyand, Jane; Hwang, E. Shelley; Estep, Anne L. H.; Chen, Yunn-Yi; Chew, Karen L.; Dairkee, Shanaz H.; Jensen, Ronald M.; Waldman, Frederic M.
CS Comprehensive Cancer Center, University of California San Francisco, San Francisco, CA, 94143-0808, USA
SO Cancer Research (2003), 63(21), 7167-7175 CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
AB Invasive lobular and ductal breast tumors have distinct histologies and clin. presentation. Other than altered expression of E-cadherin, little is known about the underlying biol. that distinguishes the tumor subtypes. We used cDNA microarrays to identify genes differentially expressed between lobular and ductal tumors. Unsupervised clustering of tumors failed to distinguish between the two subtypes. Prediction anal. for microarrays (PAM) was able to predict tumor type with an accuracy of 93.7%. Genes that were significantly differentially expressed between the two groups were identified by MaxT permutation anal. using t tests (20 cDNA clones and 10 unique genes), significance anal. for microarrays (33 cDNA clones and 15 genes, at an estd. false discovery rate of 2%), and PAM (31 cDNAs and 15 genes). There were 8 genes identified by all three of these related methods (E-cadherin, survivin, cathepsin B, TPI1, SPRY1, SCYA14, TFAP2B, and thrombospondin 4), and an addnl. 3 that were identified by significance anal. for microarrays and PAM (osteopontin, HLA-G, and CHC1). To validate the differential expression of these genes, 7 of them were tested by real-time quant. PCR, which verified that they were differentially expressed in lobular vs. ductal tumors. In conclusion, specific changes in gene expression distinguish lobular from ductal breast carcinomas. These genes may be important in understanding the basis of phenotypic differences among breast cancers.
RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 73 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:884557 CAPLUS
DN 140:123298
TI A novel design of whole-genome microarray probes for Saccharomyces cerevisiae which minimizes cross-hybridization
AU Talla, Emmanuel; Tekaia, Fredj; Brino, Laurent; Dujon, Bernard
CS Institut Pasteur, URA 2171 CNRS, UFR 927 Universite PM Curie, Paris, F-75724, Fr.
SO BMC Genomics (2003), 4, No pp. given CODEN: BGMEET; ISSN: 1471-2164 URL: http://www.biomedcentral.com/1471-2164/4/38
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Numerous DNA microarray hybridization expts. have been performed in yeast over the last years using either synthetic oligonucleotides or PCR-amplified coding sequences as probes. The design and quality of the microarray probes are of crit. importance for hybridization expts. as well as subsequent anal. of the data. We present here a novel design of Saccharomyces cerevisiae microarrays based on a refined annotation of the genome and with the aim of reducing cross-hybridization between related sequences. An effort was made to design probes of similar lengths, preferably located in the 3'-end of reading frames. The sequence of each gene was compared against the entire yeast genome and optimal sub-segments giving no predicted cross-hybridization were selected. A total of 5660 novel probes (more than 97% of the yeast genes) were designed. For the remaining 143 genes, cross-hybridization was unavoidable. Using a set of 18 deletant strains, we have expt. validated our cross-hybridization procedure. Sensitivity, reproducibility and dynamic range of these new microarrays have been measured. Based on this experience, we have written a novel program to design long oligonucleotides for microarray hybridizations of complete genome sequences. A validated procedure to predict cross-hybridization in microarray probe design was defined in this work. Subsequently, a novel Saccharomyces cerevisiae microarray (which minimizes cross-hybridization) was designed and constructed. Arrays are available at Eurogentec S. A. Finally, we propose a novel design program, OliD, which allows automatic oligonucleotide design for microarrays. The OliD program is available from authors.
RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 74 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:883695 CAPLUS
DN 140:71726
TI Kernel hierarchical gene clustering from microarray expression data
AU Qin, Jie; Lewis, Darrin P.; Noble, William Stafford
CS Columbia Genome Center, Columbia University, New York, NY, 10032, USA
SO Bioinformatics (2003), 19(16), 2097-2104 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Unsupervised anal. of microarray gene expression data attempts to find biol. significant patterns within a given collection of expression measurements. For example, hierarchical clustering can be applied to expression profiles of genes across multiple expts., identifying groups of genes that share similar expression profiles. Previous work using the support vector machine supervised learning algorithm with microarray data suggests that higher-order features, such as pairwise and tertiary correlations across multiple expts., may provide significant benefit in learning to recognize classes of co-expressed genes. We describe a generalization of the hierarchical clustering algorithm that efficiently incorporates these higher-order features by using a kernel function to map the data into a high-dimensional feature space. We then evaluate the utility of the kernel hierarchical clustering algorithm using both internal and external validation. The expts. demonstrate that the kernel representation itself is insufficient to provide improved clustering performance. We conclude that mapping gene expression data into a high-dimensional feature space is only a good idea when combined with a learning algorithm, such as the support vector machine that does not suffer from the curse of dimensionality.
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 75 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:883690 CAPLUS
DN 140:71722
TI Venn Mapping: clustering of heterologous microarray data based on the number of co-occurring differentially expressed genes
AU Smid, Marcel; Dorssers, Lambert C. J.; Jenster, Guido
CS Department of Pathology, Josephine Nefkens Inst., 3000, Neth.
SO Bioinformatics (2003), 19(16), 2065-2071 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB To evaluate microarray data, clustering is widely used to group biol. samples or genes. However, problems arise when comparing heterologous databases. As the clustering algorithm searches for similarities between expts., it will most likely first sep. the data sets, masking relationships that exist between samples from different databases. We developed a program, Venn Mapper, to calc. the statistical significance of the no. of co-occurring differentially expressed genes in any of the two expts. For proof of principle, we analyzed a heterologous data set of 170 microarrays including breast and prostate cancer microarray analyses. Significant overlap was found in an unsupervised anal. between metastasized prostate cancer and metastasized breast cancer and BRCA mutated breast cancer. A comparison between single microarray data and the averaged breast and prostate data sets was also evaluated. This anal. suggests that genes expressed higher in stromal cells are also implicated in metastatic prostate cancer and BRCA mutated breast cancer. The Venn Mapper program identifies overlaps between samples from heterologous data sets and directly exts. the genes responsible for the overlap.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 76 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:878825 CAPLUS
DN 140:54107
TI Normalization of DNA-microarray data by nonlinear correlation maximization
AU Faller, D.; Voss, H. U.; Timmer, J.; Hobohm, U.
CS Freiburg Center for Data Analysis and Modelin, Freiburg, 79104, Germany
SO Journal of Computational Biology (2003), 10(5), 751-762 CODEN: JCOBEM; ISSN: 1066-5277
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB Signal data from DNA-microarray ("chip") technol. can be noisy; i.e., the signal variation of one gene on a series of repetitive chips can be substantial. It is becoming more and more recognized that a sufficient no. of chip replicates has to be made in order to sep. correct from incorrect signals. To reduce the systematic fraction of the noise deriving from pipetting errors, from different treatment of chips during hybridization, and from chip-to-chip manufg. variability, normalization schemes are employed. We present here an iterative nonparametric nonlinear normalization scheme called simultaneous alternating conditional expectation (sACE), which is designed to maximize correlation between chip repeats in all-chip-against-all space. We tested sACE on 28 expts. with 158 Affymetrix one-color chips. The procedure should be equally applicable to other DNA-microarray technologies, e.g., two-color chips. We show that the redn. of noise compared to a simple normalization scheme like the widely used linear global normalization leads to fewer false-pos. calls, i.e., to fewer genes which have to be laboriously confirmed by independent methods such as TaqMan or quant. PCR.
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 77 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:864283 CAPLUS
DN 140:88639
TI Selection and validation of microarray candidate genes from subregions and subnuclei of the brain
AU Zirlinger, Mariela
CS Department of Molecular and Cellular Biology, Harvard University, Cambridge, MA, 02138, USA
SO Methods (San Diego, CA, United States) (2003), 31(4), 290-300 CODEN: MTHDE9; ISSN: 1046-2023

PB Elsevier Science
DT Journal
LA English
AB DNA array technol. now allows an enormous amt. of expression data to be obtained. For large-scale gene profiling enterprises, this is of course welcome. However, the scientist interested in follow-up studies of a handful of differentially expressed genes may find it hard to sift through the vast datasets to pinpoint genes with the most desirable and reliable behaviors. Here, we present the methodol. we have employed to discover genes differentially expressed in the adult mouse brain. We first used Affymetrix microarrays to compare gene expression from five different brain regions: the amygdala, cerebellum, hippocampus, olfactory bulb, and periaqueductal gray. Second, we identified genes differentially expressed within three distinct amygdala subnuclei. In this case, the tissue was microdissected by laser-capture to minimize contamination from adjacent subnuclei, and extd. RNA was subjected to three rounds of linear amplification prior to hybridization to the microarrays. To select candidate genes, we developed a custom algorithm to identify those genes with the most robust changes in expression across different replicate samples. Confirmation of expression patterns with in situ hybridization uncovered further criteria to consider in the selection process.
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 78 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:864282 CAPLUS
DN 140:71701
TI Using ANOVA for gene selection from microarray studies of the nervous system
AU Pavlidis, Paul
CS Department of Biomedical Informatics and Columbia Genome Center, Columbia University, New York, NY, 10032, USA
SO Methods (San Diego, CA, United States) (2003), 31(4), 282-289 CODEN: MTHDE9; ISSN: 1046-2023
PB Elsevier Science
DT Journal
LA English
AB Methods are presented for detecting differential expression using statistical hypothesis testing methods including anal. of variance (ANOVA). Practicalities of exptl. design, power, and sample size are discussed. Methods for multiple testing correction and their application are described. Instructions for running typical analyses are given in the R programming environment. R code and the sample data set used to generate the examples are available at http://microarray.cpmc.columbia.edu/pavlidis/pub/aovmethods/.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 79 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:864280 CAPLUS
DN 140:71700
TI Normalization of cDNA microarray data
AU Smyth, Gordon K.; Speed, Terry
CS Walter and Eliza Hall Institute, Parkville, 3050, Australia
SO Methods (San Diego, CA, United States) (2003), 31(4), 265-273 CODEN: MTHDE9; ISSN: 1046-2023
PB Elsevier Science
DT Journal
LA English
AB Normalization means to adjust microarray data for effects which arise from variation in the technol. rather than from biol. differences between the RNA samples or between the printed probes. This paper describes normalization methods based on the fact that dye balance typically varies with spot intensity and with spatial position on the array. Print-tip loess normalization provides a well-tested general purpose normalization method which has given good results on a wide range of arrays. The method may be refined by using quality wts. for individual spots. The method is best combined with diagnostic plots of the data which display the spatial and intensity trends. When diagnostic plots show that biases still remain in the data after normalization, further normalization steps such as plate-order normalization or scale-normalization between the arrays may be undertaken. Composite normalization may be used when control spots are available which are known to be not differentially expressed. Variations on loess normalization include global loess normalization and two-dimensional normalization. Detailed commands are given to implement the normalization techniques using freely available software.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 80 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:862464 CAPLUS
DN 140:420038
TI On-line microfluidic sensor integrated with a micro array electrode and enzyme-modified pre-reactor for the real-time monitoring of blood catecholamine
AU Hayashi, Katsuyoshi; Iwasaki, Yuzuru; Kurita, Ryoji; Sunagawa, Kenji; Niwa, Osamu
CS NTT Microsystem Integration Laboratories, Atsugi, Kanagawa, Wakamiya, 243-0198, Japan
SO Electrochemistry Communications (2003), 5(12), 1037-1042 CODEN: ECCMF9; ISSN: 1388-2481
PB Elsevier Science B.V.
DT Journal
LA English
AB The authors developed an online microfluidic sensing device with an interdigitated array (IDA) electrode and a micro pre-reactor for the real-time monitoring of blood catecholamine (CA) and succeeded in the highly sensitive detection of dopamine (DA) in the presence of L-ascorbic acid (AA). The authors' device exhibits the lowest detection limit (110 .+-. 10 pM (S/N = 3)), of reported catecholamine sensors. The improvement in sensitivity results from the high redox cycling of DA and the increase in the mass transfer rate per unit time onto the IDA electrode achieved by the flow measurement. The pre-reactor was integrated upstream in the micro flow channel to eliminate AA. A large no. of rectangular shaped micropillars, which were modified with ascorbate oxidase, were formed in the pre-reactor to increase the surface area. The flow was disturbed by the two dimensional micropillar arrangement. This structure enables us to increase the elimination efficiency for AA. As a result, we achieved both the continuous and highly selective detection of 1 nM DA with complete elimination of 10 .mu.M AA in the sample soln. without employing any selective membrane such as Nafion, whose use reduces sensitivity due to the low diffusion coeff. of DA inside the membrane.
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 81 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:851030 CAPLUS
DN 140:210989
TI In vivo multi-tissue corticosteroid microarray time series available online at Public Expression Profile Resource (PEPR)
AU Almon, Richard R.; Chen, Josephine; Snyder, Grayson; DuBois, Debra C.; Jusko, William J.; Hoffman, Eric P.
CS Department of Biological Sciences, SUNY at Buffalo, Buffalo, NY, 14260, USA
SO Pharmacogenomics (2003), 4(6), 791-799 CODEN: PARMFL; ISSN: 1462-2416
PB Ashley Publications Ltd.
DT Journal
LA English
AB Gene microarrays are becoming a key tool for the anal. of changes in gene expression in a variety of conditions. Use of microarrays to analyze drug responses has mainly been restricted to comparing treated vs. untreated samples at a few time points. Such data do not permit the use of another important tool, pharmacokinetic/pharmacodynamic (PK/PD) modeling. Such modeling requires the simultaneous anal. of pharmacokinetic data along with time series data on dynamic responses. This report describes data obtained from two extended microarray time series (rat liver and skeletal muscle) for the in vivo responses to a single bolus dose of methylprednisolone that are uniquely available online in a single gene query format. Use of these data does not require any a priori knowledge or software normally necessary for the anal. of microarray data. Since the pharmacokinetic data and receptor model have been published, the results are amenable to PK/PD and pharmacogenomic evaluation.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 82 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:842948 CAPLUS
DN 139:375812
TI wCLUTO: A web-enabled clustering toolkit
AU Rasmussen, Matthew D.; Deshpande, Mukund S.; Karypis, George; Johnson, James; Crow, John A.; Retzel, Ernest F.
CS Department of Computer Science and Engineering, University of Minnesota, Minneapolis, MN, 55455, USA
SO Plant Physiology (2003), 133(2), 510-516 CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Biologists
DT Journal
LA English
AB As structural and functional genomics efforts provide the biol. community with ever-broadening sets of interrelated data, the need to explore such complex information for subtle relationships expands. We present wCLUTO, a Web-enabled version of the stand-alone application CLUTO, designed to apply clustering methods to genomic information. Its first application is focused on the clustering transcriptome data from microarrays. Data can be uploaded by the user into the clustering tool, a choice of several clustering methods can be made and configured, and data are presented to the user in a variety of visual formats, including a three-dimensional "mountain" view of the clusters. Parameters can be explored to rapidly examine a variety of clustering results, and the resulting clusters can be downloaded either for manipulation by other programs or to be saved in a format for publication.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 83 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:824794 CAPLUS
DN 139:391872
TI Automatic registration of microarray images. II. Hexagonal grid
AU Galinsky, Vitaly L.
CS Illumina, Inc., San Diego, CA, 92121, USA
SO Bioinformatics (2003), 19(14), 1832-1836 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB In the first part of this paper the author presented an efficient, robust and completely automated algorithm for spot and block indexing in microarray images with rectangular grids. Although the rectangular grid is currently the most common type of grouping the probes on microarray slides, there is another microarray technol. based on bundles of optical fibers where the probes are packed in hexagonal grids. The hexagonal grid provides both advantages and drawbacks over the std. rectangular packing and of course requires adaptation and/or modification of the algorithm of spot indexing presented in the first part of the paper. In the second part of the paper the

author presents a version of the spot indexing algorithm adapted for microarray images with spots packed in hexagonal structures. The algorithm is completely automated, works with hexagonal grids of different types and with different parameters of grid spacing and rotation as well as spot sizes. It can successfully trace the local and global distortions of the grid, including non-orthogonal transformations. Similar to the algorithm from part I, it scales linearly with the grid size, the time complexity is O(M), where M is total no. of grid points in hexagonal grid. The algorithm has been tested both on CCD and scanned images with spot expression rates as low as 2%. The processing time of an image with about 50 000 hex grid points was less than a second. For images with high expression rates (.apprx.90%) the registration time is even smaller, around a quarter of a second.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 84 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:824790 CAPLUS
DN 140:23739
TI A tool-kit for cDNA microarray and promoter analysis
AU Shah, N. H.; King, D. C.; Shah, P. N.; Fedoroff, N. V.
CS The Huck Institute of Life Sciences, PA, 16802, USA
SO Bioinformatics (2003), 19(14), 1846-1848 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB We describe two sets of programs for expediting routine tasks in anal. of cDNA microarray data and promoter sequences. The first set permits bad data points to be flagged with respect to a no. of parameters and performs normalization in three different ways. It allows combining of result files into comprehensive data sets, evaluation of the quality of both tech. and biol. replicates and row and/or column standardization of data matrixes. The second set supports mapping ESTs in the genome, identifying the corresponding genes and recovering their promoters, analyzing promoters for transcription factor binding sites, and visual representation of the results. The programs are designed primarily for Arabidopsis thaliana researchers, but can be adapted readily for other model systems.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 85 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:824772 CAPLUS
DN 140:13665
TI Transformation and normalization of oligonucleotide microarray data
AU Geller, Sue C.; Gregg, Jeff P.; Hagerman, Paul; Rocke, David M.
CS Department of Mathematics, Texas A&M University, College Station, TX, 77843-3368, USA
SO Bioinformatics (2003), 19(14), 1817-1823 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Most methods of analyzing microarray data or doing power calcns. have an underlying assumption of const. variance across all levels of gene expression. The most common transformation, the logarithm, results in data that have const. variance at high levels but not at low levels. Rocke and Durbin showed that data from spotted arrays fit a two-component model and Durbin, Hardin, Hawkins, and Rocke, Huber et al. and Munson provided a transformation that stabilizes the variance as well as symmetrizes and normalizes the error structure. We wish to evaluate the applicability of this transformation to the error structure of GeneChip microarrays. We demonstrate in an example study a simple way to use the two-component model of Rocke and Durbin and the data transformation of Durbin, Hardin, Hawkins and Rocke, Huber et al. and Munson on Affymetrix GeneChip data. In addn. we provide a method for normalization of Affymetrix GeneChips simultaneous with the detn. of the transformation, producing a data set without chip or slide effects but with const. variance and with sym. errors. This transformation/normalization process can be thought of as a machine calibration in that it requires a few biol. const. replicates of one sample to det. the const. needed to specify the transformation and normalize. It is hypothesized that this const. needs to be found only once for a given technol. in a lab, perhaps with periodic updates. It does not require extensive replication in each study. Furthermore, the variance of the transformed pilot data can be used to do power calcns. using std. power anal. programs.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 86 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:824766 CAPLUS
DN 139:391870
TI Controlling false-negative errors in microarray differential expression analysis: a PRIM approach
AU Cole, Steve W.; Galic, Zoran; Zack, Jerome A.
CS Department of Medicine, UCLA AIDS Inst., Los Angeles, CA, USA
SO Bioinformatics (2003), 19(14), 1808-1816 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Theor. considerations suggest that current microarray screening algorithms may fail to detect many true differences in gene expression (Type II analytic errors). We assessed 'false neg.' error rates in differential expression analyses by conventional linear statistical models (e.g. t-test), microarray-adapted variants (e.g. SAM, Cyber-T), and a novel strategy based on hold-out cross-validation. The latter approach employs the machine-learning algorithm Patient Rule Induction Method (PRIM) to infer min. thresholds for reliable change in gene expression from Boolean conjunctions of fold-induction and raw fluorescence measurements. Monte Carlo analyses based on four empirical data sets show that conventional statistical models and their microarray-adapted variants overlook more than 50% of genes showing significant up-regulation. Conjoint PRIM prediction rules recover approx. twice as many differentially expressed transcripts while maintaining strong control over false-pos. (Type I) errors. As a result, exptl. replication rates increase and total analytic error rates decline. RT-PCR studies confirm that gene inductions detected by PRIM but overlooked by other methods represent true changes in mRNA levels. PRIM-based conjoint inference rules thus represent an improved strategy for high-sensitivity screening of DNA microarrays.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 87 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:819231 CAPLUS
DN 140:36589
TI Representational oligonucleotide microarray analysis: A high-resolution method to detect genome copy number variation
AU Lucito, Robert; Healy, John; Alexander, Joan; Reiner, Andrew; Esposito, Diane; Chi, Maoyen; Rodgers, Linda; Brady, Amy; Sebat, Jonathan; Troge, Jennifer; West, Joseph A.; Rostan, Seth; Nguyen, Ken C. Q.; Powers, Scott; Ye, Kenneth Q.; Olshen, Adam; Venkatraman, Ennapadam; Norton, Larry; Wigler, Michael
CS Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 11724, USA
SO Genome Research (2003), 13(10), 2291-2305 CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB We have developed a methodol. we call ROMA (representational oligonucleotide microarray anal.), for the detection of the genomic aberrations in cancer and normal humans. By arraying oligonucleotide probes designed from the human genome sequence, and hybridizing with "representations" from cancer and normal cells, we detect regions of the genome with altered "copy no.". We achieve an av. resoln. of 30 kb throughout the genome, and resolns. as high as a probe every 15 kb are practical. We illustrate the characteristics of probes on the array and accuracy of measurements obtained using ROMA. Using this methodol., we identify variation between cancer and normal genomes, as well as between normal human genomes. In cancer genomes, we readily detect amplifications and large and small homozygous and hemizygous deletions. Between normal human genomes, we frequently detect large (100 kb to 1 Mb) deletions or duplications. Many of these changes encompass known genes. ROMA will assist in the discovery of genes and markers important in cancer, and the discovery of loci that may be important in inherited predispositions to disease.
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 88 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:807883 CAPLUS
DN 140:36585
TI MProbe: ***computer*** aided probe design for oligonucleotide ***microarrays***
AU Li, Wuju; Huang, Jian; Fan, Ming; Wang, Shenqi
CS Beijing Institute of Basic Medical Sciences, Beijing, Peop. Rep. China
SO Applied Bioinformatics (2002), 1(3), 163-166 CODEN: ABPIC8; ISSN: 1175-5636
PB Open Mind Journals
DT Journal
LA English
AB The present work describes a complete probe design software system for oligonucleotide microarrays based on Kane's research on probe sensitivity and specificity (Kane's rule). Combining Kane's rule and traditional criteria for probe design we constructed MProbe, the software system for oligonucleotide microarrays using Java. The general criteria for probe design are: (1) probes may have different lengths that range from 20 to 100 bases; (2) they should have a similar melting temp. (Tm) or GC content; (3) they should not contain stable secondary structures; and (4) they abide by Kane's rule.
RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 89 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:807879 CAPLUS
DN 140:402732
TI TAD: a web interface and database for tissue microarrays
AU Coombes, Kevin R.; Zhang, Lin; Bueso-Ramos, Carlos; Brisbay, Shawn; Logothetis, Christopher; Roth, Jack; Keating, Michael J.; McDonnell, Timothy J.
CS Department of Biostatistics, The University of Texas MD Anderson Cancer Center, Houston, TX, USA
SO Applied Bioinformatics (2002), 1(3), 155-158 CODEN: ABPIC8; ISSN: 1175-5636
PB Open Mind Journals
DT Journal
LA English
AB Tissue microarrays are increasingly important tools that bring high-throughput technol. to traditional pathol. labs. In many cases, each spot on a tissue microarray is scored by a skilled pathologist and recorded manually. TAD consists of an Active Server Page web interface to a relational database that automates recording scores and linking them with clin. data for future interpretation. TAD is an open source application that can be installed locally.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 90 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:804603 CAPLUS
DN 140:36577

TI A software package for cDNA microarray data normalization and assessing confidence intervals
AU Hyduke, Daniel R.; Rohlin, Lars; Kao, Katy C.; Liao, James C.
CS Department of Chemical Engineering, University of California at Los Angeles, CA, USA
SO OMICS (2003), 7(3), 227-234 CODEN: OMICAE; ISSN: 1536-2310
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB DNA microarray data are affected by variations from a no. of sources. Before these data can be used to infer biol. information, the extent of these variations must be assessed. Here we describe an open source software package, lcDNA, that provides tools for filtering, normalizing, and assessing the statistical significance of cDNA microarray data. The program employs a hierarchical Bayesian model and Markov Chain Monte Carlo simulation to est. gene-specific confidence intervals for each gene in a cDNA microarray data set. This program is designed to perform these primary anal. operations on data from two-channel spotted, or in situ synthesized, DNA microarrays.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 91 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:799448 CAPLUS
DN 140:36570
TI Combining gene expression and molecular marker information for mapping complex trait genes: a simulation study
AU Perez-Enciso, Miguel; Toro, Miguel A.; Tenenhaus, Michel; Gianola, Daniel
CS Station d'Amelioration Genetique des Animaux, INRA, Castanet-Tolosan, 31326, Fr.
SO Genetics (2003), 164(4), 1597-1606 CODEN: GENTAE; ISSN: 0016-6731
PB Genetics Society of America
DT Journal
LA English
AB A method for mapping complex trait genes using cDNA ***microarray*** and mol. marker data jointly is presented and illustrated via ***simulation*** . We introduce a novel approach for ***simulating*** phenotypes and genotypes conditionally on real, publicly available, ***microarray*** data. The model assumes an underlying continuous latent variable (liability) related to some measured cDNA expression levels. Partial least-squares logistic regression is used to est. the liability under several scenarios where the level of gene interaction, the gene effect, and the no. of cDNA levels affecting liability are varied. The results suggest that: (1) the usefulness of microarray data for gene mapping increases when both the no. of cDNA levels in the underlying liability and the QTL effect decrease and when genes are coexpressed; (2) the correlation between estd. and true liability is large, at least under our simulation settings; (3) it is unlikely that cDNA clones identified as significant with partial least squares (or with some other technique) are the true responsible cDNAs, esp. as the no. of clones in the liability increases; (4) the no. of putatively significant cDNA levels increases critically if cDNAs are coexpressed in a cluster (however, the proportion of true causal cDNAs within the significant ones is similar to that in a no-coexpression scenario); and (5) data redn. is needed to smooth out the variability encountered in expression levels when these are analyzed individually.
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 92 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:797726 CAPLUS
DN 140:351241
TI Kinetics of hybridization on the oligonucleotide microchips with gel pads
AU Sorokin, N. V.; Chechetkin, V. R.; Livshits, M. A.; Vasiliskov, V. A.; Turygin, A. Y.; Mirzabekov, A. D.
CS Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, 119991, Russia
SO Journal of Biomolecular Structure & Dynamics (2003), 21(2), 279-288 CODEN: JBSDD6; ISSN: 0739-1102
PB Adenine Press
DT Journal
LA English
AB The kinetics of hybridization on the oligonucleotide microchip with gel pads is studied both theor. and exptl. The monitoring of kinetics was performed with the measurements of fluorescence intensity produced by the labeled target oligonucleotides. As is shown, the hybridization time depends on the stability of the formed duplexes, the concns. of target and probe oligonucleotides, and the diffusion of target oligonucleotides in soln. and gel pad. The initial stage of hybridization is detd. by the flow of target oligonucleotides from soln., then, followed by the diffusive propagation with approx. const. concn. of oligonucleotides at the boundary of gel pad and, finally, by the exponential satn. The theor. predictions of hybridization kinetics reveal a good correspondence with the exptl. results and may be used for the choice of the optimal hybridization conditions. The possible applications of kinetic hybridization curves to the discrimination problems and assessment of diffusion coeffs. in gel pads are briefly discussed. Finally, we discuss the relationships between the binding kinetics and the general functioning of biomol. microchips.
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 93 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:791034 CAPLUS
DN 140:36424
TI Comparison and meta-analysis of ***microarray*** data: from the bench to the ***computer*** desk
AU Moreau, Yves; Aerts, Stein; De Moor, Bart; De Strooper, Bart; Dabrowski, Michal
CS Department of Electrical Engineering ESAT-SCD, Katholieke Universiteit Leuven, Heverlee (Leuven), 3001, Belg.
SO Trends in Genetics (2003), 19(10), 570-577 CODEN: TRGEE2; ISSN: 0168-9525
PB Elsevier Science Ltd.
DT Journal; General Review
LA English
AB A review. The upcoming availability of public microarray repositories and of large compendia of gene expression information opens up a new realm of possibilities for microarray data anal. An essential challenge is the efficient integration of microarray data generated by different research groups on different array platforms. This review focuses on the problems assocd. with this integration, which are: (1) the efficient access to and exchange of microarray data; (2) the validation and comparison of data from different platforms (cDNA and short and long oligonucleotides); and (3) the integrated statistical anal. of multiple data sets.
RE.CNT 70 THERE ARE 70 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 94 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:778411 CAPLUS
DN 139:346410
TI Extending the utility of gene profiling data by bridging microarray platforms
AU Ferl, Gregory Z.; Timmerman, John M.; Witte, Owen N.
CS Biocybernetics Laboratory, University of California, Los Angeles, CA, 90095, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2003), 100(19), 10585-10587 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal; General Review
LA English
AB A review. In a recent issue of PNAS, Wright et al. proposed a statistical model that can be used to translate exptl. results across microarray platforms. The model is based on a linear predictor score (LPS) applied to hierarchical clustering results. The model was used to reanalyze oligonucleotide microarray data from a previous study of diffuse large B cell lymphoma tumors, and sep. the tumor samples into three groups corresponding to distinct clin. outcomes. Cross-validation of gene expression results among data sets generated in particular types of cancer by using methods such as those described by Wright et al. should help to define the genes most relevant for disease classification, prognostics, and therapeutic targeting.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 95 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:767344 CAPLUS
DN 139:333750
TI ChipCheck-A program predicting total hybridization equilibria for DNA binding to small oligonucleotide microarrays
AU Siegmund, Karsten H.; Steiner, Ulrich E.; Richert, Clemens
CS Institute for Organic Chemistry, University of Karlsruhe (TH), Karlsruhe, D-76128, Germany
SO Journal of Chemical Information and Computer Sciences (2003), 43(6), 2153-2162 CODEN: JCISD8; ISSN: 0095-2338
PB American Chemical Society
DT Journal
LA English
AB Presented here is the program ChipCheck that allows the computation of total hybridization equil. for hybridization expts. involving small oligonucleotide arrays. The calcn. requires the free energies of binding for all pairs of probes and targets as well as total strand concns. and probe mol. nos. ChipCheck has been tested computationally on microarrays with up to 100 spots and 42 target strands (4200 binding equil.). It arrives at solns. through iterations employing the multidimensional Newton method. While currently running in simulation mode only, an extension of the approach to the exhaustive anal. of chip results is being outlined and may be implemented in the future. The output displays the extent of correct and cross hybridization both graphically and numerically. In principle, calcg. total hybridization equil. allows for eliminating noise from DNA chip results and thus an improvement in sensitivity and accuracy.
RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 96 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:749061 CAPLUS
DN 139:359311
TI Microarray probe expression measures, data normalization and statistical validation
AU Saviozzi, Silvia; Calogero, Raffaele A.
CS Department of Biological and Clinical Sciences, University of Torino, Orbassano, 10043, Italy
SO Comparative and Functional Genomics (2003), 4(4), 442-446 CODEN: CFGOAT; ISSN: 1531-6912
PB John Wiley & Sons Ltd.
DT Journal; General Review
LA English
AB A review. DNA microarray technol. is a high-throughput method for gaining information on gene function. Microarray technol. is based on deposition/synthesis, in an ordered manner, on a solid surface, of thousands of EST sequences/genes/oligonucleotides. Due to the high no. of generated datapoints, computational tools are essential in microarray data anal. and mining to grasp knowledge from exptl. results. In this review, we will focus on some of the methodologies actually available to define gene expression intensity measures, microarray data normalization, and statistical validation of differential expression.

RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 97 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:748577 CAPLUS
DN 140:1517
TI A dynamic approach to mapping coordinates between microplates and microarrays
AU Cheung, Kei-Hoi; Hager, Janet; Nelson, Kenneth; White, Kevin; Li, Yuli; Snyder, Michael; Williams, Kenneth; Miller, Perry
CS Department of Anesthesiology, Center for Medical Informatics, Yale University, New Haven, CT, 06520, USA
SO Journal of Biomedical Informatics (2003), Volume Date 2002, 35(5/6), 306-312 CODEN: JBIOBL; ISSN: 1532-0464
PB Elsevier Science
DT Journal
LA English
AB The retrieval of useful data from spotted microarray slides requires keeping track of which microplate wells and DNA sample corresponds to each spot on each array slide. Existing approaches are closely coupled with the type of arrayer in use and are computer operating-system-specific. To support the ***microarray*** researcher community at large who use different arrayers and ***computer*** platforms, increased flexibility, generality, and portability of these approaches are required. In this paper, we describe a general algorithm that correlates the well positions of DNA samples in each microplate to the positions of the spots on each array slide. Based on this algorithm, we have implemented a flexible and platform-independent program named MicroArray Convolutor (MAC). MAC provides a Web soln. allowing the user to import a text file that identifies the DNA samples and their well locations and to select a transformation method that converts data in 96-well plate format into 384-well plate format. It also specifies the output format of the array lists dependant on the configuration of the array platform as well as the downstream anal. software chosen for the array. MAC and its source code can be accessed via the following Web address: http://ymd.med.yale.edu/kei- cgi/kc_mac_dev8.pl.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 98 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:737258 CAPLUS
DN 139:242529
TI Use of DNA microarrays for gene expression profiling or detection of single nucleotide polymorphisms associated with disease and methods for diagnosis
IN Fukushima, Kazuhisa; Tanaami, Takeo
PA Yokogawa Electric Corporation, Japan
SO U.S. Pat. Appl. Publ., 9 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2003175782 A1 20030918 US 2003-384706 20030311 JP 2003271735 A2 20030926 JP 2002-67252 20020312
PRAI JP 2002-67252 A 20020312
AB The present invention relates to the use of DNA microarrays for gene expression profiling or detection of single nucleotide polymorphisms assocd. with disease and methods for diagnosis. Gene expression, gene representation, or the SNPs of genes, from samples of blood, bodily fluids, or affected parts collected from patients are analyzed and stored in a database. With such a system configuration as described above, it is possible to perform the preprocessing of the aforementioned samples and gene detection within the same container and the anal. of the resulting data is performed without interruption and completed within an hour.

L6 ANSWER 99 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:736521 CAPLUS
DN 139:323066
TI GenoMap, a circular genome data viewer
AU Sato, Naoki; Ehira, Shigeki
CS Department of Molecular Biology, Faculty of Science, Saitama University, Saitama, 338-8570, Japan
SO Bioinformatics (2003), 19(12), 1583-1584 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB A Tcl/Tk-based application called GenoMap, a viewer for genome-wide map of microarray expression data within a circular bacterial genome, is described. An interactive interface facilitates easy identification of the expressed region. This software is also used for drawing genome-wide quant. data.
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 100 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:729417 CAPLUS
DN 139:375641
TI Demystified . . . tissue microarray technology
AU Packeisen, J.; Korsching, E.; Herbst, H.; Boecker, W.; Buerger, H.
CS Department of Pathology, Klinikum Osnabrueck, Osnabrueck, 49076, Germany
SO Molecular Pathology (2003), 56(4), 198-204 CODEN: MOPAF6; ISSN: 1366-8714
PB BMJ Publishing Group
DT Journal; General Review
LA English
AB A review. Several "high throughput methods" have been introduced into research and routine labs. during the past decade. Providing a new approach to the anal. of genomic alterations and RNA or protein expression patterns, these new techniques generate a plethora of new data in a relatively short time, and promise to deliver clues to the diagnosis and treatment of human cancer. Along with these revolutionary developments, new tools for the interpretation of these large sets of data became necessary and are now widely available. Tissue microarray (TMA) technol. is one of these new tools. It is based on the idea of applying miniaturization and a high throughput approach to the anal. of intact tissues. The potential and the scientific value of TMAs in modern research have been demonstrated in a logarithmically increasing no. of studies. The spectrum for addnl. applications is widening rapidly, and comprises quality control in histotechnol., longterm tissue banking, and the continuing education of pathologists. This review covers the basic tech. aspects of TMA prodn. and discusses the current and potential future applications of TMA technol.
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 101 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:725981 CAPLUS
DN 140:27423
TI SignalViewer: analyzing microarray images
AU Laws, R. J.; Bergemann, T. L.; Quiaoit, F.; Zhao, L. P.
CS Quantitative Genetic Epidemiology, Fred Hutchinson Cancer Research Center, Seattle, WA, 98109-1024, USA
SO Bioinformatics (2003), 19(13), 1716-1717 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Summary: Microarray technol. is now routinely used to monitor genome-wide expression profiles. However, current microarray imaging and anal. packages typically require manual intervention and assumptions on alignments. Unfortunately, limitations and assumptions are typically undisclosed and methods are not published. To facilitate exploration of image data, we developed SignalViewer. This paper presents a description of the application. Availability: SignalViewer is available at Supplementary information: Screenshots are available at the above location, along with downloads for Windows 2000 and Linux (Redhat 7.2).
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 102 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:718403 CAPLUS
DN 139:302645
TI Expression deconvolution: A reinterpretation of DNA microarray data reveals dynamic changes in cell populations
AU Lu, Peng; Nakorchevskiy, Aleksey; Marcotte, Edward M.
CS Institute for Cellular and Molecular Biology, University of Texas, Austin, TX, 78712-0159, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2003), 100(18), 10370-10375 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Cells grow in dynamically evolving populations, yet this aspect of expts. often goes unmeasured. A method is proposed for measuring the population dynamics of cells on the basis of their mRNA expression patterns. The population's expression pattern is modeled as the linear combination of mRNA expression from pure samples of cells, allowing reconstruction of the relative proportions of pure cell types in the population. Application of the method, termed expression deconvolution, to yeast grown under varying conditions reveals the population dynamics of the cells during the cell cycle, during the arrest of cells induced by DNA damage and the release of arrest in a cell cycle checkpoint mutant, during sporulation, and following environmental stress. Using expression deconvolution, cell cycle defects are detected and temporally ordered in 146 yeast deletion mutants; six of these defects are independently exptl. validated. Expression deconvolution allows a reinterpretation of the cell cycle dynamics underlying all previous microarray expts. and can be more generally applied to study most forms of cell population dynamics.
RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 103 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:714878 CAPLUS
DN 139:208435
TI Transformations for cDNA microarray data
AU Cui, Xiangqin; Kerr, M. Kathleen; Churchill, Gary A.
CS The Jackson Lab., USA
SO Statistical Applications in Genetics and Molecular Biology (2003), 2(1), No pp. given CODEN: SAGMCU; ISSN: 1544-6115 URL: http://www.bepress.com/cgi/viewcontent.cgi?article=1009&context=sagmb
PB Berkeley Electronic Press
DT Journal; (online computer file)
LA English
AB Two channel microarray data often contain systematic variations that can be minimized by data transformation prior to further anal. The most commonly obsd. effects are revealed by viewing scatter plots of the logarithm of the ratio by the av. logarithmic intensity of the two color channels (RI plots). In this paper we present a general model for signal intensity data with multiple error sources. We demonstrate how these sources of error influence the shape of an RI plot. We then compare some currently available transformation strategies in terms of their mechanism and performance on both ***simulated*** and real ***microarray*** data. A linlog transformation is proposed to stabilize the variance of the log ratios. We also propose a regional smoothing method to remove variation in log ratios due to spatial

heterogeneity on the microarray surface. The discussed transformations represent an important initial step in microarray data anal. for both ratio-based and ANOVA methods.
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 104 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:683044 CAPLUS
DN 139:271619
TI Shrinkage-based similarity metric for cluster analysis of microarray data
AU Cherepinsky, Vera; Feng, Jiawu; Rejali, Marc; Mishra, Bud
CS Courant Institute of Mathematical Sciences, New York University, New York, NY, 10012, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2003), 100(17), 9668-9673 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB The current std. correlation coeff. used in the anal. of microarray data was introduced by M. B. Eisen, P. T. Spellman, P. O. Brown, and D. Botstein [(1998) Proc. Natl. Acad. Sci. USA 95, 14863-14868]. Its formulation is rather arbitrary. We give a math. rigorous correlation coeff. of two data vectors based on James-Stein shrinkage estimators. We use the assumptions described by Eisen et al., also using the fact that the data can be treated as transformed into normal distributions. While Eisen et al. use zero as an estimator for the expression vector mean .mu., we start with the assumption that for each gene, .mu. is itself a zero-mean normal random variable [with a priori distribution N(0, .tau.2)]r and use Bayesian anal. to obtain a posteriori distribution of .mu. in terms of the data. The shrunk estimator for .mu. differs from the mean of the data vectors and ultimately leads to a statistically robust estimator for correlation coeffs. To evaluate the effectiveness of shrinkage, we conducted in silico expts. and also compared similarity metrics on a biol. example by using the data set from Eisen et al. For the latter, we classified genes involved in the regulation of yeast cell-cycle functions by computing clusters based on various definitions of correlation coeffs. and contrasting them against clusters based on the activators known in the literature. The estd. false positives and false negatives from this study indicate that using the shrinkage metric improves the accuracy of the anal.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 105 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:678981 CAPLUS
DN 139:192462
TI DNA microarray gene expression profile analysis data optimizations: background and bias correction via a novel mathematical model
IN Tanaka, Hiroshi; Ono, Nobukazu; Takahara, Yoshiyuki; Zhang, Quingwei
PA Ajinomoto Co., Inc., Japan
SO PCT Int. Appl., 105 pp. CODEN: PIXXD2
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2003070938 A1 20030828 WO 2003-JP1900 20030221 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
AU 2003211240 A1 20030909 AU 2003-211240 20030221
PRAI JP 2002-45407 A 20020221 WO 2003-JP1900 W 20030221
AB An app., method, computer program, and recording media for optimization of gene expression profile anal. data, are presented. Gene expression level expressed in fluorometric data, measured expt. with DNA microarrays or DNA chips, of a comparative group and a control group are cor. based on a novel mathematic model. Based on the scatter plots thus cor., a novel X-Y axis system having an x axis proportional to the fluorescence intensity of genes is constructed. Next, windows each having a definite no. of genes are made along the X-axis and the reliability limit of the arbitrary risk is detd. in each window in accordance with Student's t-distribution. Then windows are shifted by a definite no. of genes in the X-axis direction and each reliability limit is detd. The plural reliability limits thus detd. are complemented by smoothening (spline curve) to give a reliability curve of expression variation. Subsequently, genes located outside the reliability curve of expression variation thus obtained are extd. as variation genes.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 106 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:672568 CAPLUS
DN 140:299934
TI Automated acquisition of stained tissue microarrays for high-throughput evaluation of molecular targets
AU Vrolijk, Hans; Sloos, Willem; Mesker, Wilma; Franken, Patrick; Fodde, Riccardo; Morreau, Hans; Tanke, Hans
CS Laboratory for Cytochemistry and Cytometry, Department of Molecular Cell Biology, Leiden University Medical Center, Leiden, Neth.
SO Journal of Molecular Diagnostics (2003), 5(3), 160-167 CODEN: JMDIFP; ISSN: 1525-1578
PB Association for Molecular Pathology
DT Journal
LA English
AB At present, limiting factors in the use of tissue microarrays (TMAs) for high-throughput anal. relate to the visual evaluation of the staining patterns of each of the individual cores in the array and to the subsequent input of the results into a database. Such a database is essential to correlate the data with tumor type and outcome, and to evaluate the performance against other markers achieved in sep. expts. So far, these steps are mostly performed by hand, and consequently are time-consuming and potentially prone to bias and errors, resp. This paper describes the use of a high-resoln. flat-bed scanner for digitization of TMAs with a resoln. of about 5 .times. 5 .mu.m2. The arrays are acquired, the positions of the tissue cores are automatically detd., and measurement data including the images of the individual cores are archived. The program provides digital zooming of arrays for interactive verification of the results and rapid linkage of individual core images to data sets of other markers derived from the same array. Performance of the system was compared to manual classification for a representative set of arrays contg. colorectal tumors stained with different markers.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 107 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:668881 CAPLUS
DN 140:283832
TI Implementation of a redox microarray: an experimental model for future nanoscale biomolecular computing using integrated circuits
AU Hiratsuka, M.; Aoki, T.; Morimitsu, H.; Higuchi, T.
CS Sendai National College of Technology, Sendai, 989-3128, Japan
SO IEE Proceedings: Nanobiotechnology (2003), 150(1), 9-14 CODEN: IPNEAY; ISSN: 1478-1581
PB Institution of Electrical Engineers
DT Journal
LA English
AB The possibility of constructing high-d. parallel computing architectures using mol. electronics technol. is explored. By employing mol. computing devices, new circuit/system integration could be realized. To clarify the proposed concept, an exptl. model of a redox microarray is presented. A first exptl. system for a redox microarray consists of a two-dimensional array of platinum microelectrodes to catalyze reversible reactions of redox-active mols. Exptl. results of active wave propagation in the redox microarray are presented to demonstrate the potential of mol. computing devices for creating artificially programmable reaction-diffusion dynamics for specific target applications.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 108 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:662050 CAPLUS
DN 139:333699
TI Microarrays: How Many Do You Need?
AU Zien, Alexander; Fluck, Juliane; Zimmer, Ralf; Lengauer, Thomas
CS Max-Planck-Institut fuer biologische Kybernetik, Tuebingen, 72076, Germany
SO Journal of Computational Biology (2003), 10(3-4), 653-667 CODEN: JCOBEM; ISSN: 1066-5277
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB We est. the no. of microarrays that is required in order to gain reliable results from a common type of study: the pairwise comparison of different classes of samples. We show that current knowledge allows for the construction of models that look realistic with respect to searches for individual differentially expressed genes and derive prototypical parameters from real data sets. Such models allow investigation of the dependence of the required no. of samples on the relevant parameters: the biol. variability of the samples within each class, the fold changes in expression that are desired to be detected, the detection sensitivity of the microarrays, and the acceptable error rates of the results.
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 109 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:662045 CAPLUS
DN 139:333697
TI Set association analysis of SNP case-control and microarray data
AU Ott, Jurg; Hoh, Josephine
CS Rockefeller University, New York, NY, 10021, USA
SO Journal of Computational Biology (2003), 10(3-4), 569-574 CODEN: JCOBEM; ISSN: 1066-5277
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB Common heritable diseases ("complex traits") are assumed to be due to multiple underlying susceptibility genes. While genetic mapping methods for Mendelian disorders have been very successful, the search for genes underlying complex traits has been difficult and often disappointing. One of the reasons may be that most current gene-mapping approaches are still based on conventional methodol. of testing one or a few SNPs at a time. Here, we demonstrate a simple strategy that allows for the joint anal. of multiple disease-assocd. SNPs in different genomic regions. Our set-assocn. method combines information over SNPs by forming sums of relevant single-marker statistics. As previously hypothesized, we show here that this approach successfully addresses the "curse of dimensionality" problem- too many variables should be estd. with a comparatively small no. of observations. We also report results

of simulation studies showing that our method furnishes unbiased and accurate significance levels. Power calcns. demonstrate good power even in the presence of large nos. of nondisease assocd. SNPs. We extended our method to microarray expression data, where expression levels for large nos. of genes should be compared between two tissue types. In applications to such data, our approach turned out to be highly efficient.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 110 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:655744 CAPLUS
DN 139:243934
TI Binarization of microarray data on the basis of a mixture model
AU Zhou, Xiaobo; Wang, Xiaodong; Dougherty, Edward R.
CS Department of Electrical Engineering, Texas A and M University, College Station, TX, 77843, USA
SO Molecular Cancer Therapeutics (2003), 2(7), 679-684 CODEN: MCTOCF; ISSN: 1535-7163
PB American Association for Cancer Research
DT Journal
LA English
AB Although gathered as continuous data, expression measurements from gene microarrays may be quantized before downstream anal. and modeling. This is esp. true for modeling gene prediction and genetic regulatory networks. Coarse quantization results in lower computational requirements, lower data requirements for model inference, and easier conceptualization. This paper proposes a mixt. model for binarization. For each gene, the model, composed of a sum of two distributions, is fit to expression data for that gene, and data points are binarized according to the model. The mixt. model is based on the assumption of multiplicative up-regulation. The proposed method is compared with mean and median binarization by comparing classification performance based on the binary data from the different methods. Classification is performed for ***simulated*** data generated from a ***microarray*** model studied previously and for cancer data arising from two studies involving hereditary breast cancer and small, round blue-cell tumors of childhood.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 111 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:648962 CAPLUS
DN 139:255937
TI Room-Temperature Single-Nucleotide Polymorphism and Multiallele DNA Detection Using Fluorescent Nanocrystals and Microarrays
AU Gerion, Daniele; Chen, Fanqing; Kannan, Balaji; Fu, Aihua; Parak, Wolfgang J.; Chen, David J.; Majumdar, Arunava; Alivisatos, A. Paul
CS Department of Chemistry and Department of Mechanical Engineering, University of California, Berkeley, CA, 94720, USA
SO Analytical Chemistry (2003), 75(18), 4766-4772 CODEN: ANCHAM; ISSN: 0003-2700
PB American Chemical Society
DT Journal
LA English
AB We report two cDNA microarray-based applications of DNA-nanocrystal conjugates, single-nucleotide polymorphism (SNP) and multiallele detections, using a com. scanner and two sets of nanocrystals with orthogonal emissions. We focus on SNP mutation detection in the human p53 tumor suppressor gene, which has been found to be mutated in more than 50% of the known human cancers. DNA-nanocrystal conjugates are able to detect both SNP and single-base deletion at room temp. within minutes, with true-to-false signal ratios above 10. We also demonstrate microarray-based multiallele detection, using hybridization of multicolor nanocrystals conjugated to two sequences specific for the hepatitis B and hepatitis C virus, two common viral pathogens that inflict more than 10% of the population in the developing countries worldwide. The simultaneous detection of multiple genetic markers with microarrays and DNA-nanocrystal conjugates has no precedent and suggests the possibility of detecting an even greater no. of bacterial or viral pathogens simultaneously.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 112 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:643328 CAPLUS
DN 139:242407
TI Determination of binding constants on microarrays with confocal fluorescence detection
AU Elbs, Martin; Brock, Roland
CS Institute for Cell Biology, University of Tuebingen, Tuebingen, 72076, Germany
SO Analytical Chemistry (2003), 75(18), 4793-4800 CODEN: ANCHAM; ISSN: 0003-2700
PB American Chemical Society
DT Journal
LA English
AB Confocal laser scanning microscopy was employed for the detn. of binding consts. of receptor-ligand interactions in a microarray format. Protocols for a localized immobilization of amine contg. substances on glass via GOPTS (3-glycidyloxypropyl)trimethoxysilane were optimized with respect to the detection of ligand binding by fluorescence. Compatibility with miniaturization by nanopipetting devices was ensured during all steps. The interaction of the tripeptide L-Lys-D-Ala-D-Ala with vancomycin immobilized on glass served as a model. To minimize consumption of ligand, binding consts. were detd. by stepwise titrn. of binding sites. The binding const. of the unlabeled ligand was detd. by competitive titrn. with a fluorescently labeled analog. The detd. binding consts. agreed well with those detd. by other techniques, previously. Labeled ligand bound stronger than the unlabeled one. This difference was dye-dependent. Still, binding was specific for the tripeptide moiety confirming that ligand and fluorescent analog competed for the same binding sites these results validate the detn. of binding consts. by competitive titrn. The protocols established for confocal fluorescence detection are applicable to axially resolved detection modalities and screening for unlabeled ligands by competitive titrn. in general.
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 113 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:622610 CAPLUS
DN 139:287238
TI Statistical implication of pooling RNA samples for microarray experiments
AU Peng, Xuejun; Wood, Constance L.; Blalock, Eric M.; Chen, KueyChu; Landfield, Philip W.; Stromberg, Arnold J.
CS Department of Statistics, University of Kentucky, Lexington, KY, 40506, USA
SO BMC Bioinformatics (2003), 4, No pp. given CODEN: BBMIC4; ISSN: 1471-2105
URL: http://www.biomedcentral.com/content/pdf/1471-2105-4-26.pdf
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Microarray technol. has become a very important tool for studying gene expression profiles under various conditions. Biologists often pool RNA samples extd. from different subjects onto a single microarray chip to help defray the cost of microarray expts. as well as to correct for the tech. difficulty in getting sufficient RNA from a single subject. However, the statistical, tech. and financial implications of pooling have not been explicitly investigated. Modeling the resulting gene expression from sample pooling as a mixt. of individual responses, we derived expressions for the exptl. error and provided both upper and lower bounds for its value in terms of the variability among individuals and the no. of RNA samples pooled. Using "virtual" pooling of data from real expts. and computer simulations, we investigated the statistical properties of RNA sample pooling. Our study reveals that poolingbiol. samples appropriately is statistically valid and efficient for microarray expts. Furthermore, optimal pooling design(s) can be found to meet statistical requirements while minimizing total cost. Appropriate RNA pooling can provide equiv. power and improve efficiency and cost-effectiveness for microarray expts. with a modest increase in total no. of subjects. Pooling schemes in terms of replicates of subjects and arrays can be compared before expts. are conducted.
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 114 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:619792 CAPLUS
DN 139:225431
TI Graphical methods for class prediction using dimension reduction techniques on DNA microarray data
AU Bura, Efstathia; Pfeiffer, Ruth M.
CS Department of Statistics, The George Washington University, Washington, DC, 20052, USA
SO Bioinformatics (2003), 19(10), 1252-1258 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB We introduce simple graphical classification and prediction tools for tumor status using geneexpression profiles. They are based on two dimension estn. techniques sliced av. variance estn. (SAVE) and sliced inverse regression (SIR). Both SAVE and SIR are used to infer on the dimension of the classification problem and obtain linear combinations of genes that contain sufficient information to predict class membership, such as tumor type. Plots of the estd. directions as well as numerical thresholds estd. from the plots are used to predict tumor classes in cDNA microarrays and the performance of the class predictors is assessed by cross-validation. A ***microarray*** ***simulation*** study is carried out to compare the power and predictive accuracy of the two methods. The methods are applied to cDNA microarray data on BRCA1 and BRCA2 mutation carriers as well as sporadic tumors from Hedenfalk et al. (2001). All samples are correctly classified.
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 115 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:619790 CAPLUS
DN 139:240939
TI Estimating the occurrence of false positives and false negatives in microarray studies by approximating and partitioning the empirical distribution of p-values
AU Pounds, Stan; Morris, Stephan W.
CS Department of Biostatistics, St. Jude Children's Research Hospital, Memphis, TN, 38105-2794, USA
SO Bioinformatics (2003), 19(10), 1236-1242 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB The occurrence of false positives and false negatives in a microarray anal. could be easily estd. if the distribution of p-values were approximated and then expressed as a mixt. of null and alternative densities. Essentially any distribution of p-values can be expressed as such a mixt. by extg. a uniform d. from it. A model is introduced that frequently describes very accurately the distribution of a set of p-values arising from an array anal. The model is used to obtain an estd. distribution that is easily expressed as

a mixt. of null and alternative densities. Given a threshold of significance, the estd. distribution is partitioned into regions corresponding to the occurrences of false positives, false negatives, true positives, and true negatives.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 116 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:616887 CAPLUS
DN 139:257649
TI A model-based analysis of microarray experimental error and normalization
AU Fang, Yongxiang; Brass, Andrew; Hoyle, David C.; Hayes, Andrew; Bashein, Abdulla; Oliver, Stephen G.; Waddington, David; Rattray, Magnus
CS School of Biological Sciences, University of Manchester, Manchester, M13 9PT, UK
SO Nucleic Acids Research (2003), 31(16), e96/1-e96/13 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB A statistical model is proposed for the anal. of errors in microarray expts. and is employed in the anal. and development of a combined normalization regime. Through anal. of the model and two-dye microarray data sets, this study found the following. The systematic error introduced by microarray expts. mainly involves spot intensity-dependent, feature-specific and spot position-dependent contributions. It is difficult to remove all these errors effectively without a suitable combined normalization operation. Adaptive normalization using a suitable regression technique is more effective in removing spot intensity-related dye bias than self-normalization, while regional normalization (block normalization) is an effective way to correct spot position-dependent errors. However, dye-flip replicates are necessary to remove feature-specific errors, and also allow the analyst to identify the exptl. introduced dye bias contained in non-self-self data sets. In this case, the bias present in the data sets may include both exptl. introduced dye bias and the biol. difference between two samples. Self-normalization is capable of removing dye bias without identifying the nature of that bias. The performance of adaptive normalization, on the other hand, depends on its ability to correctly identify the dye bias. If adaptive normalization is combined with an effective dye bias identification method then there is no systematic difference between the outcomes of the two methods.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 117 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:600340 CAPLUS
DN 139:174771
TI Design and implementation of integrated system for microarray data
AU Lee, Mi-Kyung; Choi, Jeong-Hyeon; Cho, Hwan-Gue
CS Department of computer Science, Pusan National University, Pusan, S. Korea
SO Han'guk Misaengmul-Saengmyongkong Hakhoechi (2003), 31(2), 182-190 CODEN: HMHAAS
PB Korean Society for Microbiology and Biotechnology
DT Journal
LA Korean
AB As DNA microarrays are widely used recently, the amt. of microarray data is exponentially increasing. Until now, however, no domestic system is available for the efficient management of such data. Because the no. of exptl. data in a specific lab. is limited, it is necessary to avoid redundant expts. and to accumulate the results using a shared data management system for microarrays. In this paper, a system named WEMA (WEb management of MicroArrays) was designed and implemented to manage and process the microarray data. WEMA system was designed to include the basic feature of MIAME (Minimal Information About a Microarray Expt.), and general data units were also defined in the system in order to systematically manage the data. The WEMA system has three main features: efficient management of microarray data, integration of input/ouput data, and metafile processing. The system was tested with actual microarray data produced by a mol. biol. lab., and we found that the biologists could systematically manage and easily analyze the microarray data. As a consequence, the researchers could reduce the cost of data exchange and communication.

L6 ANSWER 118 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:599902 CAPLUS
DN 139:255909
TI Spurious spatial periodicity of co-expression in microarray data due to printing design
AU Balazsi, Gabor; Kay, Krin A.; Barabasi, Albert-Laszlo; Oltvai, Zoltan N.
CS Feinberg School of Medicine, Department of Pathology, Northwestern University, Chicago, IL, 60611, USA
SO Nucleic Acids Research (2003), 31(15), 4425-4433 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB Global transcriptome data is increasingly combined with sophisticated math. analyses to ext. information about the functional state of a cell. Yet the extent to which the results reflect exptl. bias at the expense of true biol. information remains largely unknown. Here we show that the spatial arrangement of probes on microarrays and the particulars of the printing procedure significantly affect the log-ratio data of mRNA expression levels measured during the Saccharomyces cerevisiae cell cycle. We present a numerical method that filters out these technol.-derived contributions from the existing transcriptome data, leading to improved functional predictions. The example presented here underlines the need to routinely search and compensate for inherent exptl. bias when analyzing systematically collected, internally consistent biol. data sets.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 119 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:579645 CAPLUS
DN 139:255887
TI 2HAPI: a microarray data analysis system
AU Fink, J. Lynn; Drewes, Scott; Patel, Hiren; Welsh, John B.; Masys, Daniel R.; Corbeil, Jacques; Gribskov, Michael
CS San Diego Supercomputer Center, San Diego, CA, 92093-0537, USA
SO Bioinformatics (2003), 19(11), 1443-1445 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB 2HAPI (version 2 of High d. Array Pattern Interpreter) is a web-based, publicly-available anal. tool designed to aid researchers in microarray data anal. 2HAPI includes tools for searching, manipulating, visualizing, and clustering the large sets of data generated by microarray expts. Other features include assocn. of genes with NCBI information and linkage to external data resources. Unique to 2HAPI is the ability to retrieve upstream sequences of co-regulated genes for promoter anal. using MEME (Multiple Expectation-maximization for Motif Elicitation). 2HAPI is freely available at http://array.sdsc.edu.
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 120 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:579631 CAPLUS
DN 139:255881
TI Quantitative quality control in microarray experiments and the application in data filtering, normalization and false positive rate prediction
AU Wang, Xujing; Hessner, Martin J.; Wu, Yan; Pati, Nirupma; Ghosh, Soumitra
CS Department of Pediatrics, Max McGee National Research Center for Juvenile Diabetes, Medical College and Children's Hospital of Wisconsin, Milwaukee, WI, 53226, USA
SO Bioinformatics (2003), 19(11), 1341-1347 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Data preprocessing including proper normalization and adequate quality control before complex data mining is crucial for studies using the cDNA microarray technol. We have developed a simple procedure that integrates data filtering and normalization with quant. quality control of microarray expts. Previously we have shown that data variability in a microarray expt. can be very well captured by a quality score qcom that is defined for every spot, and the ratio distribution depends on qcom. Utilizing this knowledge, our data-filtering scheme allows the investigator to decide on the filtering stringency according to desired data variability, and our normalization procedure corrects the qcom-dependent dye biases in terms of both the location and the spread of the ratio distribution. In addn., we propose a statistical model for false pos. rate detn. based on the design and the quality of a microarray expt. The model predicts that a lower limit of 0.5 for the replicate concordance rate is needed in order to be certain of true positives. Our work demonstrates the importance and advantages of having a quant. quality control scheme for microarrays.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 121 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:579629 CAPLUS
DN 139:255880
TI New normalization methods for cDNA microarray data
AU Wilson, D. L.; Buckley, M. J.; Helliwell, C. A.; Wilson, I. W.
CS CSIRO Mathematical and Information Sciences, Australia
SO Bioinformatics (2003), 19(11), 1325-1332 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB The focus of this paper is on two new normalization methods for cDNA microarrays. After the image anal. has been performed on a microarray and before differentially expressed genes can be detected, some form of normalization must be applied to the microarrays. Normalization removes biases towards one or other of the fluorescent dyes used to label each mRNA sample allowing for proper evaluation of differential gene expression. The two normalization methods that we present here build on previously described non-linear normalization techniques. We extend these techniques by firstly introducing a normalization method that deals with smooth spatial trends in intensity across microarrays, an important issue that must be dealt with. Secondly we deal with normalization of a new type of cDNA microarray expt. that is coming into prevalence, the small scale specialty or boutique' array, where large proportions of the genes on the microarrays are expected to be highly differentially expressed. The normalization methods described in this paper are available via http://www.pi.csiro.au/gena/ in a software suite called tRMA.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 122 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:575279 CAPLUS
DN 139:192146
TI A mixture model-based cluster analysis of DNA microarray gene expression data on brahman and brahman composite steers fed high-, medium-, and low-quality diets
AU Reverter, A.; Byrne, K. A.; Bruce, H. L.; Wang, Y. H.; Dalrymple, B. P.; Lehnert, S. A.

CS Cooperative Research Centre for Cattle and Beef Quality, Queensland Bioscience Precinct, CSIRO Livestock Industries, St Lucia, 4067, Australia
SO Journal of Animal Science (Savoy, IL, United States) (2003), 81(8), 1900-1910 CODEN: JANSAG; ISSN: 0021-8812
PB American Society of Animal Science
DT Journal
LA English
AB The objective of this study is to explore aspects of the statistical anal. of gene expression response at the muscle tissue level to varying levels of energy and protein in the diet. Eleven Brahman and Brahman composite steers (weighing 302 .+-. 9.8 kg, on av.) were allocated randomly into high- (HIGH), medium- (MED), and low- (LOW) quality forage diets for 27 d. After this period, a biopsy of the longissimus dorsi muscle was taken from each animal and total RNA was extd. to generate the labeled target for microarray experimentation. These targets were hybridized to a complementary DNA (cDNA) microarray of 9,274 probes from cattle muscle and s.c. fat cDNA libraries. After edits, 151,904 expression intensity levels of 4,747 genes were analyzed. Emphasis was given to the choice of power transformation of the intensity channel readings and to the consistency of readings within each diet quality group. The statistical approach to isolate differentially expressed genes was based on model-based clustering via a mixt. of normal distributions estd. through maximal likelihood. The base-2 logarithm was found to be the optimal power transformation to normalize gene intensity levels. A two-sample t-statistic was defined as a measure of possible differential expression. For each of the three diet contrasts, HIGH vs. LOW, HIGH vs. MED, and MED vs. LOW, three clusters were found, two of which contained more than 94% genes with almost no altered gene expression levels, whereas the third cluster contained the remaining genes with a differential expression. Results from the HIGH vs. LOW contrast identified 27 genes with a greater than 95% posterior probability of belonging to the cluster of differentially expressed genes.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 123 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:551086 CAPLUS
DN 139:81667
TI Method system and ***computer*** program product for quality assurance in detecting biochemical markers by ***microarrays*** of imaging
IN Barrus, Jeffrey K.; Ryan, John Henry
PA Myriad Genetics, Inc., USA
SO U.S. Pat. Appl. Publ., 35 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2003134320 A1 20030717 US 2003-345905 20030115
PRAI US 2002-349165P P 20020115
AB A method is disclosed for providing a certified biochem. profile of a biol. sample. The biochem. profile includes a plurality of data objects for a plurality of mol. markers. The method comprises: (1) providing a first data set for the plurality of mol. markers of the biol. sample by a first process from a first elec. signal representing a first unprocessed image data; (2) providing a second data set for said plurality of mol. markers of the biol. sample by a second process from a second elec. signal representing a second unprocessed image data, wherein the first process is different from said second process; and (3) comparing, by a computer-readable program code, the first and second data sets, whereby a certified biochem. profile is generated if no discrepancy between the first and second data sets are detected. Preferably, the steps of the method are coordinated by another computer-readable program code. Systems and computer program products embodying the method or useful in the method are also disclosed.

L6 ANSWER 124 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:521887 CAPLUS
DN 139:174416
TI Modeling of DNA microarray data by using physical properties of hybridization
AU Held, G. A.; Grinstein, G.; Tu, Y.
CS IBM Thomas J. Watson Research Center, Yorktown Heights, NY, 10598, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2003), 100(13), 7575-7580 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB A method of analyzing DNA microarray data based on the phys. modeling of hybridization is presented. We demonstrate, in exptl. data, a correlation between obsd. hybridization intensity and calcd. free energy of hybridization. Then, combining hybridization rate equations, calcd. free energies of hybridization, and microarray data for known target concns., we construct an algorithm to compute transcript concn. levels from microarray data. We also develop a method for eliminating outlying data points identified by our algorithm. We test the efficacy of these methods by comparing our results with an existing statistical algorithm, as well as by performing a cross-validation test on our model.
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 125 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:511949 CAPLUS
DN 139:48149
TI Imaging microarrays
IN Piper, James R.
PA Vysis, Inc., USA
SO U.S. Pat. Appl. Publ., 27 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2003124589 A1 20030703 US 2002-269723 20021011 WO 2003030620 A2 20030417 WO 2002-US32523 20021011 WO 2003030620 A3 20031106 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2001-328760P P 20011012
AB A method of obtaining a cor. image of a microarray includes acquiring an image of a microarray including a target spot, and processing the image to correct for background noise and chip misalignment. The method also includes analyzing the image to identify a target patch, edit debris, and correct for ratio bias; and detecting single copy no. variation in the target spot using an objective statistical anal. that includes a t-value statistical anal. The method provides statistically robust computational processes for accurately detecting genomic variation at the single copy level.

L6 ANSWER 126 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:508036 CAPLUS
DN 139:160734
TI Use of mixture models in a microarray-based screening procedure for detecting differentially represented yeast mutants
AU Irizarry, Rafael; Wu, Zhijin; Ooi, Siew Loon; Boeke, Jef D.
CS Johns Hopkins University, USA
SO Statistical Applications in Genetics and Molecular Biology (2003), 2(1), No pp. given CODEN: SAGMCU; ISSN: 1544-6115 URL: http://www.bepress.com/cgi/viewcontent.cgi?article=1002&context=sagmb
PB Berkeley Electronic Press
DT Journal; (online computer file)
LA English
AB We describe the use of a statistical model in a genome-wide microarray-based yeast genetic screen performed by imposing different genetic selections on thousands of yeast mutants in parallel. A mixt. model is fitted to data obtained from oligonucleotide arrays hybridized to 20-mer oligonucleotide "barcodes" and a procedure based on the fitted model is used to search for mutants differentially represented under exptl. and control conditions. The fitted stochastic model provides a way to assess uncertainty. We demonstrate the usefulness of the model by applying it to the problem of screening for components of the nonhomologous end joining (NHEJ) pathway and identified known components of the NHEJ pathway.
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 127 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:508030 CAPLUS
DN 139:174767
TI Pre-validation and inference in microarrays
AU Tibshirani, Robert J.; Efron, Brad
CS Stanford University, USA
SO Statistical Applications in Genetics and Molecular Biology (2002), 1(1), No pp. given CODEN: SAGMCU; ISSN: 1544-6115 URL: http://www.bepress.com/cgi/viewcontext.cgi?article=1000&content=sagmb
PB Berkeley Electronic Press
DT Journal; (online computer file)
LA English
AB In microarray studies, an important problem is to compare a predictor of disease outcome derived from gene expression levels to std. clin. predictors. Comparing them on the same dataset that was used to derive the microarray predictor can lead to results strongly biased in favor of the microarray predictor. The authors propose a new technique called "pre-validation" for making a fairer comparison between the two sets of predictors. The authors study the method anal. and explore its application in a recent study on breast cancer.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 128 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:506371 CAPLUS
DN 139:145923
TI Gene analysis using DNA microarrays
AU Paweletz, Cloud P.; Bichsel, Verena E.; Liotta, Lance A.
CS Department of Chemistry, Georgetown University, Washington, DC, USA
SO Progress in Oncology (2001) 1-15, 2 plates CODEN: PORNAF; ISSN: 1535-9980
PB Jones and Bartlett Publishers
DT Journal; General Review
LA English
AB A review. The ***computerized*** strategies of the gene anal. for DNA ***microarrays*** were described. The outlined flow of the anal. processes of the cDNA microarrays anal., transcriptional profiling anal. of cancers, and gene expression arrays anal. of microdissected tissue samples was discussed.
RE.CNT 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 129 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:501135 CAPLUS
DN 139:144560
TI GenePublisher: automated analysis of DNA microarray data
AU Knudsen, Steen; Workman, Christopher; Sicheritz-Ponten, Thomas; Friis, Carsten
CS Center for Biological Sequence Analysis, BioCentrum-DTU, Lyngby, 2800, Den.
SO Nucleic Acids Research (2003), 31(13), 3471-3476 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB GenePublisher, a system for automatic anal. of data from DNA microarray expts., has been implemented with a web interface. Raw data are uploaded to the server together with a specification of the data. The server performs normalization, statistical anal. and visualization of the data. The results are run against databases of signal transduction pathways, metabolic pathways and promoter sequences in order to ext. more information. The results of the entire anal. are summarized in report form and returned to the user.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 130 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:501134 CAPLUS
DN 139:144909
TI ExpressYourself: a modular platform for processing and visualizing microarray data
AU Luscombe, Nicholas M.; Royce, Thomas E.; Bertone, Paul; Echols, Nathaniel; Horak, Christine E.; Chang, Joseph T.; Snyder, Michael; Gerstein, Mark
CS Department of Molecular Biophysics and Biochemistry, Yale University, New Haven, CT, 06520-8114, USA
SO Nucleic Acids Research (2003), 31(13), 3477-3482 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB DNA microarrays are widely used in biol. research; by analyzing differential hybridization on a single microarray slide, one can detect changes in mRNA expression levels, increases in DNA copy nos. and the location of transcription factor binding sites on a genomic scale. Having performed the expts., the major challenge is to process large, noisy datasets in order to identify the specific array elements that are significantly differentially hybridized. This normally requires aggregating different, often incompatible programs into a multi-step pipeline. Here the authors present ExpressYourself, a fully integrated platform for processing microarray data. In completely automated fashion, it will correct the background array signal, normalize the Cy5 and Cy3 signals, score levels of differential hybridization, combine the results of replicate expts., filter problematic regions of the array and assess the quality of individual and replicate expts. ExpressYourself is designed with a highly modular architecture so various types of microarray anal. algorithms can readily be incorporated as they are developed; for example, the system currently implements several normalization methods, including those that simultaneously consider signal intensity and slide location. The processed data are presented using a web-based graphical interface to facilitate comparison with the original images of the array slides. In particular, Express Yourself is able to regenerate images of the original microarray after applying various steps of processing, which greatly facilities identification of position-specific artifacts. The program is freely available for use at http://bioinfo.mbb.yale.edu/express yourself.
RE.CNT 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 131 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:501128 CAPLUS
DN 139:160491
TI Design of oligonucleotides for microarrays and perspectives for design of multi-transcriptome arrays
AU Nielsen, Henrik Bjorn; Wernersson, Rasmus; Knudsen, Steen
CS BioCentrum-DTU, Center for Biological Sequence Analysis, Technical University of Denmark, Lyngby, 2800, Den.
SO Nucleic Acids Research (2003), 31(13), 3491-3496 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB Optimal design of oligonucleotides for microarrays involves tedious and laborious work evaluating potential oligonucleotides relative to a series of parameters. The currently available tools for this purpose are limited in their flexibility and do not present the oligonucleotide designer with an overview of these parameters. We present here a flexible tool named OligoWiz for designing oligonucleotides for multiple purposes. OligoWiz presents a set of parameter scores in a graphical interface to facilitate an overview for the user. Addnl. custom parameter scores can easily be added to the program to extend the default parameters: homol., .DELTA.Tm, low-complexity, position and GATC-only. Furthermore we present an anal. of the limitations in designing oligonucleotide sets that can detect transcripts from multiple organisms.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 132 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:501097 CAPLUS
DN 139:128674
TI GEPAS: a web-based resource for microarray gene expression data analysis
AU Herrero, Javier; Al-Shahrour, Fatima; Diaz-Uriarte, Ramon; Mateos, Alvaro; Vaquerizas, Juan M.; Santoyo, Javier; Dopazo, Joaquin
CS Bioinformatics Unit, Centro Nacional de Investigaciones Oncologicas (CNIO), Madrid, 28029, Spain
SO Nucleic Acids Research (2003), 31(13), 3461-3467 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB We present a web-based pipeline for microarray gene expression profile anal., GEPAS, which stands for Gene Expression Profile Anal. Suite (). GEPAS is composed of different interconnected modules which include tools for data pre-processing, two-conditions comparison, unsupervised and supervised clustering (which include some of the most popular methods as well as home made algorithms) and several tests for differential gene expression among different classes, continuous variables or survival anal. A multiple purpose tool for data mining, based on Gene Ontol., is also linked to the tools, which constitutes a very convenient way of analyzing clustering results. Online tutorials are available at http://bioinfo.cnio.es.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 133 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:488015 CAPLUS
DN 140:177482
TI Design and analysis of microcantilevers for biosensing applications
AU Zhang, Xuan; Yang, Mo; Vafai, Kambiz; Ozkan, Cengiz S.
CS University of California-Riverside, USA
SO JALA (2003), 8(2), 90-93 CODEN: JALLFO; ISSN: 1535-5535
PB Association for Laboratory Automation
DT Journal
LA English
AB We have analyzed the detection of microcantilevers utilized in biosensing chips. First, the primary deflection due to the chem. reaction between the analyte mols. and the receptor coating, which produces surface stresses on the receptor side is analyzed. Oscillating flow conditions, which are the main source of turbulence in cantilever based biosensing chips, are found to produce substantial deflections in the microcantilever at relatively large frequency of turbulence. Then mech. design and optimization of piezoresistive cantilevers for biosensing applications is studied. Models are described for predicting the static behavior of cantilevers with elastic and piezoresistive layers. Chemo-mech. binding forces have been analyzed to understand issues of satn. over the cantilever surface. Furthermore, the introduction of stress concn. regions during cantilever fabrication has been discussed which greatly enhances the detection sensitivity through increased surface stress, and novel microcantilever assemblies are presented for the first time that can increase the deflection due to chem. reaction. Finally an expt. was made to demonstrate the shift of resonant frequency of cantilever used as biosensor. The relation between resonant frequency shift and the surface stress was analyzed.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 134 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:483048 CAPLUS
DN 139:240907
TI Expression profiles in the progression of ductal carcinoma in the breast
AU Lattimore, B. Samuel; Crabbe, M. James C.
CS Department of Animal and Microbial Sciences, Division of Cell and Molecular Biology, University of Reading, Whiteknights, Reading, Berkshire, RG6 6AJ, UK
SO Computational Biology and Chemistry (2003), 27(2), 115-120 CODEN: CBCOCH; ISSN: 1476-9271
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB An understanding of the multi-step nature of cancer as it is in the breast, as a series of pivotal genetic/epigenetic modifications is irrefutably a milestone in diagnostics, prognostics and eventually providing a cure. Here we have utilized a variant of anal. of variance (ANOVA) as a model for the identification and tracking of specific mRNA species whose transcription has been significantly altered at each grade in the progression of ductal carcinoma, making it possible to correlate histol. progression with the genetic events underlying breast cancer. We show that in the progression of ductal carcinomas, from grade 1 to 3, there is a redn. in the actual no. of mRNA species, which are significantly over or under expressed. We also show that this technique can be employed to generate differential gene expression patterns, whereby the combined expression profile of the tailored spectra of genes in the comparison of each ductal grade is sufficient to render them on clearly sep. arms of an array-wise hierarchical cluster dendrogram.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 135 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:479936 CAPLUS
DN 139:129056
TI Improved gene selection for classification of microarrays
AU Jaeger, J.; Sengupta, R.; Ruzzo, W. L.
CS Department of Computer Science & Engineering, University of Washington, Seattle, WA, 98195, USA
SO Pacific Symposium on Biocomputing 2003, Kauai, HI, United States, Jan. 3-7, 2003 (2003), 53-64. Editor(s): Altman, Russ B. Publisher: World Scientific Publishing Co. Pte. Ltd., Singapore, Singapore. CODEN: 69ECRC; ISBN: 981-238-217-8
DT Conference

LA English
AB In this paper we derive a method for evaluating and improving techniques for selecting informative genes from microarray data. Genes of interest are typically selected by ranking genes according to a test-statistic and then choosing the top k genes. A problem with this approach is that many of these genes are highly correlated. For classification purposes it would be ideal to have distinct but still highly informative genes. We propose three different pre-filter methods - two based on clustering and one based on correlation - to retrieve groups of similar genes. For these groups we apply a test-statistic to finally select genes of interest. We show that this filtered set of genes can be used to significantly improve existing classifiers.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 136 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:472618 CAPLUS
DN 139:31765
TI Method, computer programs and systems for the statistical analysis of differential gene expression using a pairwise comparison of two different samples
IN Lin, Jing-zhong; Haudenschild, Christian D.; Naire, Ramesh V.; Bowen, Benjamin A.
PA Lynx Therapeutics, Inc., USA
SO PCT Int. Appl., 57 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2003050264 A2 20030619 WO 2002-US39650 20021210 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2001-341030P P 20011211
AB This invention relates to statistical anal. of differential gene expression data using a pairwise comparison of two different samples wherein each sample generates greater than 150,000 mRNA mols. Methods, computer programs and systems are provided for the anal. and comparison of gene frequency distributions generated by one or more replicate samples or by independent sampling procedures. To det. differential gene expression in a sample compared to another sample(s), the level of expression of a given mRNA in a given sample is detd. For example, the level of expression of any single gene in a dataset is calcd. by dividing the no. of signatures from that gene by the total no. of signatures for all mRNAs present in the dataset. The level of expression of a particular mRNA in one sample is statistically compared to the level of expression of the same particular mRNA in another sample. Provided is a statistical test of significance which is a normal approxn. test, which comprises a two-tailed test for the total no. of signature sequences generated from mRNA mols. in the first and second samples by massively parallel signature sequencing (MPSS).

L6 ANSWER 137 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:461964 CAPLUS
DN 139:225051
TI OligoArray 2.0: design of oligonucleotide probes for DNA microarrays using a thermodynamic approach
AU Rouillard, Jean-Marie; Zuker, Michael; Gulari, Erdogan
CS Department of Chemical Engineering, University of Michigan, H.H. Dow, Ann Arbor, MI, 48109, USA
SO Nucleic Acids Research (2003), 31(12), 3057-3062 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB There is a substantial interest in implementing bioinformatics technologies that allow the design of oligonucleotides to support the development of microarrays made from short synthetic DNA fragments spotted or in situ synthesized on slides. Ideally, such oligonucleotides should be totally specific to their resp. targets to avoid any cross-hybridization and should not form stable secondary structures that may interfere with the labeled probes during hybridization. We have developed OligoArray 2.0, a program that designs specific oligonucleotides at the genomic scale. It uses a thermodn. approach to predict secondary structures and to calc. the specificity of targets on chips for a unique probe in a mixt. of labeled probes. Furthermore, OligoArray 2.0 can adjust the oligonucleotide length, according to user input, to fit a narrow Tm range compatible with hybridization requirements. Combined with on chip oligonucleotide synthesis, this program makes it feasible to perform expression anal. on a genomic scale for any organism for which the genome sequence is known. This is without relying on cDNA or oligonucleotide libraries. OligoArray 2.0 was used to design 75 764 oligonucleotides representing 26 140 transcripts from Arabidopsis thaliana. Among this set, we provide at least one specific oligonucleotide for 93% of these transcripts.
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 138 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:461877 CAPLUS
DN 139:174396
TI eXPatGen: generating dynamic expression patterns for the systematic evaluation of analytical methods
AU Michaud, Dennis J.; Marsh, Adam G.; Dhurjati, Prasad S.
CS Department of Chemical Engineering, University of Delaware, Newark, DE, 19716, USA
SO Bioinformatics (2003), 19(9), 1140-1146 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Exptl. gene expression data sets, such as those generated by microarray or gene chip expts., typically have significant noise and complicated interconnectivities that make understanding even simple regulatory patterns difficult. Given these complications, characterizing the effectiveness of different anal. techniques to uncover network groups and structures remains a challenge. Generating simulated expression patterns with known biol. features of expression complexity, diversity and interconnectivities provides a more controlled means of investigating the appropriateness of different anal. methods. A simulation-based approach can systematically evaluate different gene expression anal. techniques and provide a basis for improved methods in dynamic metabolic network reconstruction. We have developed an online ***simulator*** , called eXPatGen, to generate dynamic gene expression patterns typical of ***microarray*** expts. eXPatGen provides a quant. network structure to represent key biol. features, including the induction, repression, and cascade regulation of mRNA (mRNA). The simulation is modular such that the expression model can be replaced with other representations, depending on the level of biol. detail required by the user. Two example gene networks, of 25 and 100 genes resp., were simulated. Two std. anal. techniques, clustering and PCA anal., were performed on the resulting expression patterns in order to demonstrate how the simulator might be used to evaluate different anal. methods and provide exptl. guidance for biol. studies of gene expression.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 139 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:461873 CAPLUS
DN 139:174394
TI Gene interaction in DNA microarray data is decomposed by information geometric measure
AU Nakahara, Hiroyuki; Nishimura, Shin-ichi; Inoue, Masato; Hori, Gen; Amari, Shun-ichi
CS Lab. for Mathematical Neuroscience, RIKEN Brain Science Institute, Saitama, 351-0198, Japan
SO Bioinformatics (2003), 19(9), 1124-1131 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Given the vast amt. of gene expression data, it is essential to develop a simple and reliable method of investigating the fine structure of gene interaction. The author introduce an information geometric measure of binary random vectors and show how this measure reveals the fine structure of gene interaction. In particular, we propose an iterative procedure by using this measure (called IPIG). The procedure finds higher-order dependencies which may underlie the interaction between two genes of interest. To demonstrate the method, we investigate the interaction between the two genes of interest in the data from human acute lymphoblastic leukemia cells. The method successfully discovered biol. known findings and also selected other genes as hidden causes that constitute the interaction. The softwares are currently not available but are possibly made available in future at http://www.mns.brain.riken.go.jp/~nakahara/DNA_pub.html, where all the related information is also linked.
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 140 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:461869 CAPLUS
DN 139:174390
TI Bagging to improve the accuracy of a clustering procedure
AU Dudoit, Sandrine; Fridlyand, Jane
CS School of Public Health, Division of Biostatistics, University of California, Berkeley, Berkeley, CA, 94720-7360, USA
SO Bioinformatics (2003), 19(9), 1090-1099 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB The microarray technol. is increasingly being applied in biol. and medical research to address a wide range of problems such as the classification of tumors. An important statistical question assocd. with tumor classification is the identification of new tumor classes using gene expression profiles. Essential aspects of this clustering problem include identifying accurate partitions of the tumor samples into clusters and assessing the confidence of cluster assignments for individual samples. Two new resampling methods, inspired from bagging in prediction, are proposed to improve and assess the accuracy of a given clustering procedure. In these ensemble methods, a partitioning clustering procedure is applied to bootstrap learning sets and the resulting multiple partitions are combined by voting or the creation of a new dissimilarity matrix. As in prediction, the motivation behind bagging is to reduce variability in the partitioning results via averaging. The performances of the new and existing methods were compared using ***simulated*** data and gene expression data from two recently published cancer ***microarray*** studies. The bagged clustering procedures were in general at least as accurate and often substantially more accurate than a single application of the partitioning clustering procedure. A valuable byproduct of bagged clustering are the cluster votes which can be used to assess the confidence of cluster assignments for individual observations.
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 141 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:442798 CAPLUS
DN 139:287233
TI Statistical methods for chip calibration and saturation effects in antibody-spiked gene expression data
AU Rao, J. Sunil; Li, Jingjin
CS Case Western Reserve University, Cleveland, OH, 44106 7235, USA
SO Respiratory Physiology & Neurobiology (2003), 135(2-3), 109-119 CODEN: RPNEAV; ISSN: 1569-9048
PB Elsevier Science Ltd.
DT Journal
LA English
AB Oligonucleotide microarrays are amongst, a set of technologies that allow for high throughput assessment of vast nos. of gene expressions. In order to evaluate gene expressions given detection limits, antibody spiking is often used providing one with an expression curve relating antibody treated expression and non-antibody treated expression. These curves can exhibit different functional shapes across chips and hence need to be standardized. In addn., each curve is subject to satn. effects, which are typically dealt with by extrapolating a linear fit to the subset of the data not visually subject to satn. In this paper we introduce methods for the non-parametric standardization of expression curves using univariate smoothers. We also explore parametric methods for more efficient anal. of the standardized curves. We demonstrate an alternate method of parametric anal. using a weighted linear mixed effects model that does not arbitrarily delete data beyond an obsd. satn. point; allows for natural grouping of genes and provides significantly more accurate predictions than naive linear extrapolation. Both methodologies are studied through sets of simulations.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 142 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:435913 CAPLUS
DN 139:96295
TI Sensitive Quantitative Nucleic Acid Detection Using Oligonucleotide Microarrays
AU Vainrub, Arnold; Pettitt, B. Montgomery
CS Department of Chemistry, University of Houston, Houston, TX, 77204-5003, USA
SO Journal of the American Chemical Society (2003), 125(26), 7798-7799 CODEN: JACSAT; ISSN: 0002-7863
PB American Chemical Society
DT Journal
LA English
AB We report a new theor. approach to optimize the performance and quantify the results of gene expression oligonucleotide microarrays which are widely used in biomedical research. An on-array hybridization isotherm that takes into account the screened Coulomb repulsion between the assayed nucleic acid target and the layer of surface tethered oligonucleotide probes is presented. The hybridization efficiency is found as a function of the genomic target (sequence, length, and concn.), array parameters (probe sequence and length, surface probe d.), and hybridization conditions (temp. and buffer ionic strength). We present simple relations for the hybridization signal max. and the linear dynamic detection range and show explicit criteria for optimization. The approach is based on an extension of our recently published theory (Vainrub, A.; Pettitt, B. M. Phys. Rev. E 2002, 66, art. no.-041905) which we generalize here for the cases of target depletion effects and arbitrary target length.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 143 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:435187 CAPLUS
DN 138:397352
TI Signature genes for differentiation of chronic phase and blast crisis in chronic myelogenous leukemia
IN Linsley, Peter S.; Mao, Mao; Dai, Hongyue; He, Yudong; Radich, Jerald Patrick
PA USA
SO U.S. Pat. Appl. Publ., 31 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2003104426 A1 20030605 US 2002-171581 20020614
PRAI US 2001-298914P P 20010618
AB The present invention relates to genetic markers whose expression is correlated with progression of chronic myelogenous leukemia (CML). Specifically, the invention provides 366 of markers whose expression patterns can be used to differentiate chronic phase individuals from those in blast crisis. The marker sets were identified by detg. which of .apprx.25,000 human markers had expression patterns that correlated with the conditions or indications. The invention relates to methods of using these markers to distinguish these conditions. The invention also relates to kits contg. ready-to-use ***microarrays*** and ***computer*** software for data anal. using the statistical methods disclosed herein.

L6 ANSWER 144 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:433838 CAPLUS
DN 139:63970
TI Microarray data analysis in studies of membrane transporters
AU Hu, Donglei
CS Gene Array Core Laboratory, Diabetes Center, University of California San Francisco, San Francisco, CA, USA
SO Methods in Molecular Biology (Totowa, NJ, United States) (2003), 227(Membrane Transporters), 71-84 CODEN: MMBIED; ISSN: 1064-3745
PB Humana Press Inc.
DT Journal
LA English
AB The different computational methods commonly used in microarray data anal. are described. The features of current major software packages and other tools and examples of applications of data anal. methods in studies of membrane transporters are presented.
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 145 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:424557 CAPLUS
DN 139:79735
TI DNA microarray data and contextual analysis of correlation graphs
AU Rougemont, Jacques; Hingamp, Pascal
CS TAGC, INSERM-ERM 206, Marseille, 13288, Fr.
SO BMC Bioinformatics (2003), 4, No pp. given CODEN: BBMIC4; ISSN: 1471-2105
URL: http://www.biomedcentral.com/1471-2105/4/15
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB DNA microarrays are used to produce large sets of expression measurements from which specific biol. information is sought. Their anal. requires efficient and reliable algorithms for dimensional redn., classification and annotation. We study networks of co-expressed genes obtained from DNA microarray expts. The math. concept of curvature on graphs is used to group genes or samples into clusters to which relevant gene or sample annotations are automatically assigned. Application to publicly available yeast and human lymphoma data demonstrates the reliability of the method in spite of its simplicity, esp. with respect to the small no. of parameters involved. We provide a method for automatically detg. relevant gene clusters among the many genes monitored with microarrays. The automatic annotations and the graphical interface improve the readability of the data. A C++ implementation, called Trixy, is available from http://tagc.univ-mrs.fr/bioinformatics/trixy.html.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 146 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:424230 CAPLUS
DN 139:174379
TI The creation of a microarray data analysis system and its application to HTLV-I-induced transformation
AU Fink, Jody Lynn
CS Univ. of California, San Diego, CA, USA
SO (2002) 220 pp. Avail.: UMI, Order No. DA3064443 From: Diss. Abstr. Int., B 2003, 63(9), 4049
DT Dissertation
LA English
AB Unavailable

L6 ANSWER 147 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:410080 CAPLUS
DN 140:193926
TI Modeling and experimental verification of the performance of TIRF-sensing systems for oligonucleotide microarrays based on bulk and integrated optical planar waveguides
AU Lehr, H.-P.; Brandenburg, A.; Sulz, G.
CS Fraunhofer-Institute of Physical Measurement Techniques IPM, Freiburg, D-79110, Germany
SO Sensors and Actuators, B: Chemical (2003), B92(3), 303-314 CODEN: SABCEB; ISSN: 0925-4005
PB Elsevier Science B.V.
DT Journal
LA English
AB The detection of hybridization events on oligonucleotide microarrays in real time can be performed, using the optical principle of total internal reflection fluorescence (TIRF). We have investigated and compared three TIRF-sensing configurations using two bulk and one integrated optical planar waveguide as transducer platforms for oligonucleotide microarrays, which have been brought in contact with flow cells. Based on the ray optics model, expressions were derived for the calcn. of the intensity of the CCD-camera signal generated by solved fluorophores in the flow cell vol. A noise anal. was performed and expressions for the calcn. of the detection limit of the surface fluorophore d. were derived. With a bulk optical single total internal reflection configuration a detection limit of 3.74 mols./.mu.m2, with a bulk optical multiple total internal reflection configuration a detection limit of 1.83 mols./.mu.m2 and with the integrated optical waveguide (IOW) configuration a detection limit of 0.013 mols./.mu.m2 was numerically estd. based on background data of the bulk vol. signal. The derived anal. expressions address the full system, including light source, optical waveguide and the detection unit and can serve as a tool for TIRF-system design.
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 148 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:404324 CAPLUS
DN 139:144503
TI Corrected small-sample estimation of the Bayes error
AU Brun, Marcel; Sabbagh, David; Kim, Seungchan; Dougherty, Edward R.
CS Department of Electrical Engineering, Texas A&M University, College Station, TX, 77840, USA
SO Bioinformatics (2003), 19(8), 944-951 CODEN: BOINFP; ISSN: 1367-4803

PB Oxford University Press
DT Journal
LA English
AB A major problem of pattern classification is estn. of the Bayes error when only small samples are available. One way to est. the Bayes error is to design a classifier based on some classification rule applied to sample data, est. the error of the designed classifier, and then use this est. as an est. of the Bayes error. Relative to the Bayes error, the expected error of the designed classifier is biased high, and this bias can be severe with small samples. This paper provides a correction for the bias by subtracting a term derived from the representation of the estn. error. It does so for Boolean classifiers, these being defined on binary features. Although the general theory applies to any Boolean classifier, a model is introduced to reduce the no. of parameters. A key point is that the expected correction is conservative. Properties of the cor. est. are studied via simulation. The correction applies to binary predictors because they are math. identical to Boolean classifiers. In this context the correction is adapted to the coeff. of detn., which has been used to measure nonlinear multivariate relations between genes and design genetic regulatory networks. An application using gene-expression data from a microarray expt. is provided on the website http://gspsnap.tamu.edu/smalls ample/(user:'smallsample',password:'smallsample').
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 149 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:404307 CAPLUS
DN 139:144497
TI Approximate variance-stabilizing transformations for gene-expression microarray data
AU Rocke, David M.; Durbin, Blythe
CS Department of Applied Science, University of California, Davis, Davis, CA, 95616, USA
SO Bioinformatics (2003), 19(8), 966-972 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB A variance stabilizing transformation for microarray data was recently introduced independently by several research groups. This transformation has sometimes been called the generalized logarithm or glog transformation. In this paper, we derive several alternative approx. variance stabilizing transformations that may be easier to use in some applications. We demonstrate that the started-log and the log-linear-hybrid transformation families can produce approx. variance stabilizing transformations for microarray data that are nearly as good as the generalized logarithm (glog) transformation. These transformations may be more convenient in some applications.
RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 150 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:401366 CAPLUS
DN 139:79611
TI Clustering-based approaches to discovering and visualizing microarray data patterns
AU Azuaje, Francisco
CS School of Computing and Mathematics, University of Ulster at Jordanstown, Newtownabbey, BT37 0QB, UK
SO Briefings in Bioinformatics (2003), 4(1), 31-42 CODEN: BBIMFX; ISSN: 1467-5463
PB Henry Stewart Publications
DT Journal; General Review
LA English
AB A review. This article focuses on clustering techniques for the anal. of microarray data and discusses contributions and applications for the implementation of intelligent diagnostic systems and therapy design studies. Approaches to validating and visualizing expression clustering results and software and other relevant resources to support clustering-based analyses are reviewed. Finally, this paper addresses current limitations and problems that need to be investigated for the development of an advanced generation of pattern discovery tools.
RE.CNT 74 THERE ARE 74 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 151 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:380369 CAPLUS
DN 139:95925
TI Analysis of microarray data using Z score transformation
AU Cheadle, Chris; Vawter, Marquis P.; Freed, William J.; Becker, Kevin G.
CS DNA Array Unit, Research Resources Branch, National Institute on Aging, National Institutes of Health, Baltimore, MD, 21221-6825, USA
SO Journal of Molecular Diagnostics (2003), 5(2), 73-81 CODEN: JMDIFP; ISSN: 1525-1578
PB Association for Molecular Pathology
DT Journal
LA English
AB High-throughput cDNA microarray technol. allows for the simultaneous anal. of gene expression levels for thousands of genes and as such, rapid, relatively simple methods are needed to store, analyze, and cross-compare basic microarray data. The application of a classical method of data normalization, Z score transformation, provides a way of standardizing data across a wide range of expts. and allows the comparison of microarray data independent of the original hybridization intensities. Data normalized by Z score transformation can be used directly in the calcn. of significant changes in gene expression between different samples and conditions. We used Z scores to compare several different methods for predicting significant changes in gene expression including fold changes, Z ratios, Z and t statistical tests. We conclude that the Z score transformation normalization method accompanied by either Z ratios or Z tests for significance ests. offers a useful method for the basic anal. of microarray data. The results provided by these methods can be as rigorous and are no more arbitrary than other test methods, and, in addn., they have the advantage that they can be easily adapted to std. spread-sheet programs.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 152 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:376278 CAPLUS
DN 138:365102
TI Methods for genotyping and diagnosis of disease using ***computer*** -readable storage media for ***microarray*** oligonucleotide probe design
IN Kwon, Tae-joon
PA S. Korea
SO U.S. Pat. Appl. Publ., 9 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2003092053 A1 20030515 US 2002-273789 20021018
PRAI KR 2001-71102 A 20011115
AB Provided are a ***computer*** -readable storage medium for ***microarray*** oligonucleotide probe design. The computer-readable storage medium has stored thereon a directory comprising an information on DNA, RNA, protein, and/or genome of a target gene and a second directory comprising an information on a specific region in the target gene and a third directory contg. an information on a probe for identifying the specific region. The first, second, and third directories are organized in a hierarchical structure in which the second directory is at a level lower than that of the first directory and the third directory is at a level lower than that of the second directory. These computer-readable storage media have applications in identifying mutations in genes assocd. with disease and may be used in diagnosis.

L6 ANSWER 153 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:375405 CAPLUS
DN 139:63927
TI Gene selection in arthritis classification with large-scale microarray expression profiles
AU Sha, Naijun; Vannucci, Marina; Brown, Philip J.; Trower, Michael K.; Amphlett, Gillian; Falciani, Francesco
CS Mathematical Sciences Department, University of Texas at El Paso, El Paso, TX, 79968-0514, USA
SO Comparative and Functional Genomics (2003), 4(2), 171-181 CODEN: CFGOAT; ISSN: 1531-6912
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB The use of large-scale microarray expression profiling to identify predictors of disease class has become of major interest. Beyond their impact in the clin. setting (i.e. improving diagnosis and treatment), these markers are also likely to provide clues on the mol. mechanisms underlining the diseases. In this paper we describe a new method for the identification of multiple gene predictors of disease class. The method is applied to the classification of two forms of arthritis that have a similar clin. endpoint but different underlying mol. mechanisms: rheumatoid arthritis (RA) and osteoarthritis (OA). We aim at both the classification of samples and the location of genes characterizing the different classes. We achieve both goals simultaneously by combining a binary probit model for classification with Bayesian variable selection methods to identify important genes. We find very small sets of genes that lead to good classification results. Some of the selected genes are clearly correlated with known aspects of the biol. of arthritis and, in some cases, reflect already known differences between RA and OA.
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 154 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:346563 CAPLUS
DN 140:123268
TI Robust cluster analysis of microarray gene expression data with the number of clusters determined biologically
AU Bickel, David R.
CS Office of Biostatistics and Bioinformatics, Medical College of Georgia, Augusta, GA, 30912-4900, USA
SO Bioinformatics (2003), 19(7), 818-824 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB The success of each method of cluster anal. depends on how well its underlying model describes the patterns of expression. Outlier-resistant and distribution-insensitive clustering of genes are robust against violations of model assumptions. A measure of dissimilarity that combines advantages of the Euclidean distance and the correlation coeff. is introduced. The measure can be made robust using a rank order correlation coeff. A robust graphical method of summarizing the results of cluster anal. and a biol. method of detg. the no. of clusters are also presented. These methods are applied to a public data set, showing that rank-based methods perform better than log-based methods. Software is available from http://www.davidbickel.com.
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 155 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:346560 CAPLUS
DN 139:128587
TI Selection of oligonucleotide probes for protein coding sequences
AU Wang, Xiaowei; Seed, Brian
CS Department of Molecular Biology, Massachusetts General Hospital, Boston, MA, 02114, USA
SO Bioinformatics (2003), 19(7), 796-802 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Large arrays of oligonucleotide probes have become popular tools for analyzing RNA expression. However to date most oligo collections contain poorly validated sequences or are biased toward untranslated regions (UTRs). Here we present a strategy for picking oligos for microarrays that focus on a design universe consisting exclusively of protein coding regions. We describe the constraints in oligo design that are imposed by this strategy, as well as a software tool that allows the strategy to be applied broadly. In this work we sequentially apply a variety of simple filters to candidate sequences for oligo probes. The primary filter is a rejection of probes that contain contiguous identity with any other sequence in the sample universe that exceeds a pre-established threshold length. We find that rejection of oligos that contain 15 bases of perfect match with other sequences in the design universe is a feasible strategy for oligo selection for probe arrays designed to interrogate mammalian RNA populations. Filters to remove sequences with low complexity and predicted poor probe accessibility narrow the candidate probe space only slightly. Rejection based on global sequence alignment is performed as a secondary, rather than primary, test, leading to an algorithm that is computationally efficient. Splice isoforms pose unique challenges and we find that isoform prevalence will for the most part have to be detd. by anal. of the patterns of hybridization of partially redundant oligonucleotides. The oligo design program OligoPicker and its source code are freely available at our website: seed@molbio.mgh.harvard.edu.
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 156 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:346559 CAPLUS
DN 139:133037
TI MARAN: normalizing micro-array data
AU Engelen, Kristof; Coessens, Bert; Marchal, Kathleen; De Moor, Bart
CS KULeuven, ESAT-SCD, Louvain, 3001, Belg.
SO Bioinformatics (2003), 19(7), 893-894 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB MARAN is a web-based application for normalizing microarray data. MARAN comprises a generic ANOVA model, an option for Loess fitting prior to ANOVA anal., and a module for selecting genes with significantly changing expression.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 157 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:346557 CAPLUS
DN 140:123266
TI Reconstructing the temporal ordering of biological samples using microarray data
AU Magwene, Paul M.; Lizardi, Paul; Kim, Junhyong
CS Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT, USA
SO Bioinformatics (2003), 19(7), 842-850 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Motivation: Accurate time series for biol. processes are difficult to est. due to problems of synchronization, temporal sampling and rate heterogeneity. Methods are needed that can utilize multi-dimensional data, such as those resulting from DNA microarray expts., in order to reconstruct time series from unordered or poorly ordered sets of observations. Results: We present a set of algorithms for estg. temporal orderings from unordered sets of sample elements. The techniques we describe are based on modifications of a min.-spanning tree calcd. from a weighted, undirected graph. We demonstrate the efficacy of our approach by applying these techniques to an artificial data set as well as several gene expression data sets derived from DNA microarray expts. In addn. to estg. orderings, the techniques we describe also provide useful heuristics for assessing relevant properties of sample datasets such as noise and sampling intensity, and we show how a data structure called a PQ-tree can be used to represent uncertainty in a reconstructed ordering. Availability: Academic implementations of the ordering algorithms are available as source code (in the programming language Python) on our web site, along with documentation on their use. The artificial 'jelly roll' data set upon which the algorithm was tested is also available from this web site. The publicly available gene expression data may be found at http://genome-www.stanford.edu/cellcycle/ and http://caulobacter.stanford.edu/CellCycle/.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 158 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:337718 CAPLUS
DN 138:380000
TI MatArray: A matlab toolbox for microarray data
AU Venet, David
CS I.R.I.B.H.M. - Campus Hopital Erasme, Brussels, CP 602-1070, Belg.
SO Bioinformatics (2003), 19(5), 659-660 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB The microarray technol. allows the high-throughput quantification of the mRNA level of thousands of genes under dozens of conditions, generating a wealth of data which must be analyzed using some form of computational means. A popular framework for such anal. is Matlab, a powerful computing language for which many functions have been written. However, although complex topics like neural networks or principal component anal. are freely available in Matlab, functions to perform more basic tasks like data normalization or hierarchical clustering in an efficient manner are not. The MatArray toolbox aims at filling this gap by offering efficient implementations of the most needed functions for microarray anal. The functions in the toolbox are command-line only, since it is geared toward seasoned Matlab users. Http://www.ulb.ac.be/medecine/iribhm/microarray/to olbox. Davenet@ulb.ac.be.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 159 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:337702 CAPLUS
DN 138:379988
TI Automatic analysis of DNA microarray images using mathematical morphology
AU Angulo, Jesus; Serra, Jean
CS Centre de Morphologie Mathematique, Ecole des Mines de Paris, Fontainebleau, 77305, Fr.
SO Bioinformatics (2003), 19(5), 553-562 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB DNA microarrays are an exptl. technol. which consists in arrays of thousands of discrete DNA sequences that are printed on glass microscope slides. Image anal. is an important aspect of microarray expts. The aim of this step is to reduce an image of spots into a table with a measure of the intensity for each spot. Efficient, accurate and automatic anal. of DNA spot images is essential in order to use this technol. in lab. routines. We present an automatic non-supervised set of algorithms for a fast and accurate spot data extn. from DNA microarrays using morphol. operators which are robust to both intensity variation and artifacts. The approach can be summarized as follows. Initially, a gridding algorithm yields the automatic segmentation of the microarray image into spot quadrants which are later individually analyzed. Then the anal. of the spot quadrant images is achieved in five steps. First, a prequantification, the spot size distribution law is calcd. Second, the background noise extn. is performed using a morphol. filtering by area. Third, an orthogonal grid provides the first approach to the spot locus. Fourth, the spot segmentation or spot boundaries definition is carried out using the watershed transformation. And fifth, the outline of detected spots allows the signal quantification or spot intensities extn.; in this respect, a noise model has been investigated. The performance of the algorithm has been compared with two packages: ScanAlyze and Genepix, showing its robustness and precision. A prototype system integrated in PDI32 (an image processing software for Windows) may be obtained from the authors on request.
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 160 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:328217 CAPLUS
DN 139:260677
TI A primer on the visualization of microarray data
AU Fawcett, Paul
CS Department of Biochemistry, Stanford University School of Medicine, Palo, CA, USA
SO Methods in Molecular Biology (Totowa, NJ, United States) (2003), 224(Functional Genomics), 219-234 CODEN: MMBIED; ISSN: 1064-3745
PB Humana Press Inc.
DT Journal
LA English
AB An overview and introduction to some of the software packages developed on the Brown and Botstein labs. at Stanford University for the visual display of microarray data are provided. A new tool DecCor2, designed to allow the genome-order display of aggregate microarray data, is described. The software packages briefly described include TreeView and Cluster, Promoter, and Caryoscope.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 161 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:327376 CAPLUS
DN 139:63908
TI Testing for differentially expressed genes with microarray data
AU Tsai, Chen-An; Chen, Yi-Ju; Chen, James J.
CS Division of Biometry and Risk Assessment, National Center for Toxicological Research, Food and Drug Administration, Jefferson, AR, 72079, USA
SO Nucleic Acids Research (2003), 31(9), e52/1-e52/10 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB This paper compares the type I error and power of the one- and two-sample t-tests, and the one- and two-sample permutation tests for detecting differences in gene expression between two ***microarray*** samples with replicates using Monte Carlo ***simulations*** . When data are generated from a normal distribution, type I errors and powers of the one-sample parametric t-test and one-sample permutation test are very close, as are the two-sample t-test and two-sample permutation test,

provided that the no. of replicates is adequate. When data are generated from a t-distribution, the permutation tests outperform the corresponding parametric tests if the no. of replicates is at least five. For data from a two-color dye swap expt., the one-sample test appears to perform better than the two-sample test since expression measurements for control and treatment samples from the same spot are correlated. For data from independent samples, such as the one-channel array or two-channel array expt. using ref. design, the two-sample t-tests appear more powerful than the one-sample t-tests.
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 162 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:327275 CAPLUS
DN 139:48100
TI Mining gene expression data using a novel approach based on hidden Markov models
AU Ji, Xinglai; Li-Ling, Jesse; Sun, Zhirong
CS Department of Biological Sciences and Biotechnology, Institute of Bioinformatics, Tsinghua University, Beijing, 100084, Peop. Rep. China
SO FEBS Letters (2003), 542(1-3), 125-131 CODEN: FEBLAL; ISSN: 0014-5793
PB Elsevier Science B.V.
DT Journal
LA English
AB In this work we have developed a new framework for microarray gene expression data anal. This framework is based on hidden Markov models. We have benchmarked the performance of this probability model-based clustering algorithm on several gene expression datasets for which external evaluation criteria were available. The results showed that this approach could produce clusters of quality comparable to two prevalent clustering algorithms, but with the major advantage of detg. the no. of clusters. We have also applied this algorithm to analyze published data of yeast cell cycle gene expression and found it able to successfully dig out biol. meaningful gene groups. In addn., this algorithm can also find correlation between different functional groups and distinguish between function genes and regulation genes, which is helpful to construct a network describing particular biol. assocns. Currently, this method is limited to time series data.
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 163 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:323808 CAPLUS
DN 138:286967
TI Construction of computer network by comparison of the gene expression profile
IN Wang, Renli
PA Liang, Gangyu, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 9 pp. CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI CN 1342775 A 20020403 CN 2000-126356 20000911
PRAI CN 2000-126356 20000911
AB The invention provides a method of constructing of computer network based on comparison of individual gene expression profile to that from a specific individual such as entertainer. The process consists of taking sample from individual, hybridization of the sample on a gene chip from the specific individual, data anal., and storing the data to a database for creation of network. The computer network for connection of different human group can be used for com. and individual uses.

L6 ANSWER 164 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:320961 CAPLUS
DN 139:31719
TI Spectral biclustering of microarray data: Coclustering genes and conditions
AU Kluger, Yuval; Basri, Ronen; Chang, Joseph T.; Gerstein, Mark
CS Department of Genetics, Yale University, New Haven, CT, 06520, USA
SO Genome Research (2003), 13(4), 703-716 CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB Global analyses of RNA expression levels are useful for classifying genes and overall phenotypes. Often these classification problems are linked, and one wants to find "marker genes" that are differentially expressed in particular sets of "conditions.". We have developed a method that simultaneously clusters genes and conditions, finding distinctive "checkerboard" patterns in matrixes of gene expression data, if they exist. In a cancer context, these checkerboards correspond to genes that are markedly up- or downregulated in patients with particular types of tumors. Our method, spectral biclustering, is based on the observation that checkerboard structures in matrixes of expression data can be found in eigenvectors corresponding to characteristic expression patterns across genes or conditions. In addn., these eigenvectors can be readily identified by commonly used linear algebra approaches, in particular the singular value decompn. (SVD), coupled with closely integrated normalization steps. We present a no. of variants of the approach, depending on whether the normalization over genes and conditions is done independently or in a coupled fashion. We then apply spectral biclustering to a selection of publicly available cancer expression data sets, and examine the degree to which the approach is able to identify checkerboard structures. Furthermore, we compare the performance of our biclustering methods against a no. of reasonable benchmarks (e.g., direct application of SVD or normalized cuts to raw data).
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 165 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:320164 CAPLUS
DN 138:315831
TI Methods and ***computer*** programs for image analysis of high-density synthetic DNA ***microarrays***
IN Zuzan, Harry; Johnson, Valen E.
PA Duke University, USA
SO PCT Int. Appl., 60 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2003034064 A2 20030424 WO 2002-US31281 20020930 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG AU 2002334769 A1 20030428 AU 2002-334769 20020930 US 2003087289 A1 20030508 US 2002-261570 20020930
PRAI US 2001-329023P P 20011012 WO 2002-US31281 W 20020930
AB Methods, systems, and ***computer*** program products for analyzing images of high d. ***microarray*** chips analyze the image by estg. background using a blurring kernel and/or a spatial multivariate statistical model of the background. The methods, systems, and computer program products can employ a multivariate statistical model and/or a blurring kernel to obtain more representative hybridization intensity results, particularly for pixels in boundary regions of the probe cells. The methods allow for alternative microarray configurations of nucleic acid probes and do not require the use of mismatch probes and can be independent of the type of nucleotide sequence used. Assocd. microarrays and systems are also described.

L6 ANSWER 166 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:301537 CAPLUS
DN 138:396686
TI Genotyping of hepatitis C viruses by DNA-microarray technology enhanced by bioinformatics
AU Trutnau, Hans-H.; Nolte, Manfred; Volkmann, Gerald; Drutschmann, Denja; Blohm, Dietmar
CS ISenseIt AG, Bremen, D-28359, Germany
SO BIOspektrum (2003), 9(1), 93-95 CODEN: BOSPFD; ISSN: 0947-0867
PB Spektrum Akademischer Verlag
DT Journal; General Review
LA German
AB A review. The software iOmega was presented for microarray-based detection and genotyping of hepatitis C viruses (HCV). Chip design and prepn., hybridization and evaluation, specificity of the chip design, and automated data interpretation of the HCV genotype 3 were described. Intelligent combinatorial anal. in probe design and evaluation were discussed.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 167 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:300529 CAPLUS
DN 138:298800
TI Methods, systems and computer software for gene expression data analysis
IN Hubbell, Earl A.
PA Affymetrix, Inc., USA
SO U.S. Pat. Appl. Publ., 12 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2003073125 A1 20030417 US 2002-273233 20021016
PRAI US 2001-329953P P 20011016
AB Methods, computer software and systems are provided for biol. data anal. In one embodiment, a probe logarithmic intensity error resolver is provided to analyze gene expression data obtained using multiprobes.

L6 ANSWER 168 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:296724 CAPLUS
DN 139:257454
TI Simulation of microfluidic pumping in a genomic DNA blood-processing cassette
AU Taylor, Michael T.; Nguyen, Peter; Ching, Jesus; Petersen, Kurt E.
CS Cepheid, Sunnyvale, CA, 94089-1302, USA
SO Journal of Micromechanics and Microengineering (2003), 13(2), 201-208 CODEN: JMMIEZ; ISSN: 0960-1317
PB Institute of Physics Publishing
DT Journal
LA English
AB Microfluidic cassettes that perform integrated biol. sample prepn. and DNA anal. require fluidic control and transport mechanisms built into the device. In this study, pneumatically actuated diaphragm pumps and valves were employed to achieve precise fluidic manipulation and enabled the execution of several sample-processing steps within a single cassette. However, the design of the microfluidic cassette to accomplish this multi-step fluidic protocol required a complex three-dimensional fluid path through

valves, bends, various sized passageways and a porous filter for cell capture. In order to understand the fluidic behavior in such a device, measurements were taken of the pneumatic pressure delivered to the diaphragm pump as it pushed sample through the complicated fluidic pathway. Simultaneously monitored were the resulting volumetric flow rate, and the corresponding pre- and post-filter fluid pressures. The data enabled the construction of a model that simulated the fluidic action through the device using established fluid mechanics theory that closely matched flow rate and pressure data. The ability to simulate the behavior of diaphragm pumping and resulting fluidic movements in complex microfluidic devices provides a greater comprehension of this phenomenon and a useful tool in the application to future devices for biochem. anal.
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 169 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:294043 CAPLUS
DN 139:100613
TI PGAGENE: integrating quantitative gene-specific results from the NHLBI Programs for Genomic Applications
AU Lee, Kyungjoon; Kohane, Isaac S.; Butte, Atul J.
CS Children's Hospital Informatics Program, Boston, MA, 02115, USA
SO Bioinformatics (2003), 19(6), 778-779 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB PGAGENE is a web-based gene-specific genomic data search engine, which allows users to search over 5.9 million pieces of collective genetic and genomic data from the NHLBI supported Programs for Genomic Applications. This data includes microarray measurements, SNPs, and mutations, and data may be found using symbols, parts of gene names or products, Affymetrix probe IDs, GenBank accession nos., UniGene IDs, dbSNP IDs, and others. The PGAGENE indexing agent periodically maps all publicly available gene-specific PGA data onto LocusLink using dynamically generated cross-referencing tables.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 170 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:288304 CAPLUS
DN 139:1934
TI An analysis of cancer microarrays in the pathway context using Bayesian networks
AU Minowa, Yohsuke; Goto, Susumu; Kanehisa, Minoru
CS Bioinformatics Center, Institute for Chemical Research, Kyoto University, Gokasho, Uji, Kyoto, 611-0011, Japan
SO Genome Informatics Series (2002), 13, 373-374 CODEN: GINSE9; ISSN: 0919-9454
PB Universal Academy Press
DT Journal
LA English
AB The candidate genes of multifactorial diseases were detected by analyzing quant. whole-genome gene expression data (DNA microarrays) using the Bayesian network method. Two Bayesian network models were considered, namely, one that consists of a continuous node and a discrete node, and another that addnl. includes relationships between continuous nodes. In these models, a discrete node represents extrinsic factors, and the effect of such factors in the network context is estd. The difference of the no. of significant nodes with various values of the no. of parent nodes was shown. Significant hits without network context were largely reduced as parent nodes are included. In contrast, some genes are turned out to become significant, when considering the network context.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 171 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:288211 CAPLUS
DN 138:363412
TI KnowledgeEditor: a tool for interactive modeling and analyzing biological pathways based on microarray data
AU Toyoda, Tetsuro; Hirosawa, Katsura; Konagaya, Akihiko
CS Bioinformatics Group, Genomic Science Center, RIKEN, Tsurumi, Yokohama, 230-0045, Japan
SO Genome Informatics Series (2002), 13, 244-245 CODEN: GINSE9; ISSN: 0919-9454
PB Universal Academy Press
DT Journal
LA English
AB KnowledgeEditor is a software that can be used to import a probe information from microarray data to a biomol. network and to modify a known metabolic pathway based on novel microarray expts. The drawn network on KnowledgeEditor can be exported in XML format, which is suitable to organize and share data among scientists. It also enables users to publish the modeled network on the web with the plug-in module GSCope Viewer.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 172 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:279312 CAPLUS
DN 139:1927
TI Microarray analysis as a process
AU Jensen, Susan
CS SPSS (UK) Ltd, Woking, GU21 6EB, UK
SO Practical Approach to Microarray Data Analysis (2003), 345-360. Editor(s): Berrar, Daniel P.; Dubitzky, Werner; Granzow, Martin. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69DTC9; ISBN: 1-4020-7260-0
DT Conference
LA English
AB The chapter describes the basic steps comprising a microarray data mining process. The European Union-funded Cross-Industry Std. Process for Data Mining (CRISP-DM) is used as the framework for an example of working through the anal. or mining of microarray data. CRISP-DM methodol. is detailed, complete, publicly accessible, and actively supported by various Data Mining software vendors. Establishing a framework for Data Mining that includes flexible boundaries and change, planning for testing of new algorithms, and tightening or loosening model success criteria will be important for the near future.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 173 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:279311 CAPLUS
DN 138:379818
TI Microarray software review
AU Leung, Yuk Fai; Lam, Dennis Shun Chiu; Pang, Chi Pui
CS Department of Ophthalmology and Visual Sciences, The Chinese University of Hong Kong, Peop. Rep. China
SO Practical Approach to Microarray Data Analysis (2003), 326-344. Editor(s): Berrar, Daniel P.; Dubitzky, Werner; Granzow, Martin. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69DTC9; ISBN: 1-4020-7260-0
DT Conference; General Review
LA English
AB A review on various microarray software categorized by their purposes and characteristics. These include primer/probe design, image anal., data mining, statistics, pathway reconstruction, and annotation software.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 174 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:279302 CAPLUS
DN 139:1472
TI Weighted flexible compound covariate method for classifying microarray data: a case study of gene expression level of lung cancer
AU Shyr, Yu; Kim, KyungMann
CS Division of Biostatistics, Department of Preventive Medicine, Vanderbilt University, Nashville, TN, 37232-6848, USA
SO Practical Approach to Microarray Data Analysis (2003), 186-200. Editor(s): Berrar, Daniel P.; Dubitzky, Werner; Granzow, Martin. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69DTC9; ISBN: 1-4020-7260-0
DT Conference; General Review
LA English
AB A review. The class comparison and prediction methods for microarray data, with an example from Vanderbilt lung cancer SPORE is discussed. These methods include the mutual information scoring (Info Score), weighted gene anal. (WGA), significance anal. of microarrays (SAM), and permutation t-test or F-test for identifying genes that are differentially expressed between different classes. The statistical class comparison and class prediction analyses for the microarray data may focus on the following steps: (1) Selecting the important gene patterns that perform differently among the study groups, (2) Using the class prediction model based upon the Weighted Flexible Compd. Covariate Method (WFCCM), classification tree methods, or other methods to verify if the genes selected in step one have the statistical significant prediction power on the training samples, (3) Applying the prediction model generated from step two to a set of test samples for examg. the prediction power on the test samples, and (4) Employing the agglomerative hierarchical clustering algorithm to investigate the pattern among the significant discriminator genes as well as the biol. status.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 175 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:279296 CAPLUS
DN 138:379973
TI Normalization: concepts and methods for normalizing microarray data
AU Morrison, Norman; Hoyle, David C.
CS Department of Computer Science, University of Manchester, Manchester, M13 9PL, UK
SO Practical Approach to Microarray Data Analysis (2003), 76-90. Editor(s): Berrar, Daniel P.; Dubitzky, Werner; Granzow, Martin. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69DTC9; ISBN: 1-4020-7260-0
DT Conference
LA English
AB Statistical techniques for normalization of microarray data are discussed. These techniques allow the user to ext. as much of the biol. signal from a microarray expt. as possible. Normalization methods that can be applied to both oligo- and spotted-array data are discussed.
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 176 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:244453 CAPLUS
DN 138:380285
TI Senescence gene expression-specific gene expression fingerprints reveal cell-type-dependent physical clustering of up-regulated chromosomal loci
AU Zhang, Hong; Pan, Kuang-Hung; Cohen, Stanley N.

CS Department of Genetics, Stanford University School of Medicine, Stanford, CA, 94305-5120, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2003), 100(6), 3251-3256 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Replicative senescence is the state of irreversible proliferative arrest that occurs as a concomitant of progressive telomere shortening. By using cDNA ***microarrays*** and the GABRIEL system of ***computer*** programs to apply domain-specific and procedural knowledge for data anal., the authors investigated global changes in gene transcription occurring during replicative senescence in human fibroblasts and mammary epithelial cells (HMECs). Here the authors report the identification of transcriptional "fingerprints" unique to senescence, the finding that gene expression perturbations during senescence differ greatly in fibroblasts and HMECs, and the discovery that despite the disparate nature of the chromosomal loci affected by senescence in fibroblasts and HMECs, the up-regulated loci in both types of cells show phys. clustering. This clustering, which contrasts with the random distribution of genes down-regulated during senescence or up-regulated during reversible proliferative arrest (i.e., quiescence), supports the view that replicative senescence is assocd. with alteration of chromatin structure.
RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 177 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:234438 CAPLUS
DN 138:281879
TI AVA: Visual analysis of gene expression microarray data
AU Zhou, Yihua; Liu, Jingdong
CS Bioinformatics, Monsanto Company, St. Louis, MO, 63167, USA
SO Bioinformatics (2003), 19(2), 293-294 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB AVA (Array Visual Analyzer) is a Java program that provides a graphical environment for visualization and anal. of gene expression microarray data. Together with its interactive visualization tools and a variety of built-in data anal. and filtration methods, AVA effectively integrates microarray data normalization, quality assessment, and data mining into one application. The software is freely available for academic users on request from the authors.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 178 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:234433 CAPLUS
DN 139:36033
TI QuickLIMS: facilitating the data management for DNA-microarray fabrication
AU Kokocinski, Felix; Wrobel, Gunnar; Hahn, Meinhard; Lichter, Peter
CS Department of Molecular Genetics, Deutsches Krebsforschungszentrum INF 280, Heidelberg, D-69120, Germany
SO Bioinformatics (2003), 19(2), 283-284 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB QuickLIMS is a Microsoft Access-based lab. information and management system capable of processing all information for microarray prodn. The program's operational flow is protocol-based, dynamically adapting to changes of the process. It interacts with the lab. robot and with other database systems over the network, and it represents a complete soln. for the management of the entire manufg. process.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 179 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:234421 CAPLUS
DN 138:317062
TI Combinatorial image analysis of DNA microarray features
AU Glasbey, C. A.; Ghazal, P.
CS Biomathematics and Statistics Scotland, JCMB, Edinburgh, EH9 3JZ, UK
SO Bioinformatics (2003), 19(2), 194-203 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB DNA and protein microarrays have become an established leading-edge technol. for large-scale anal. of gene and protein content and activity. The use of contact-printed microarrays has emerged as a relatively simple and cost effective method of choice, but its reliability is esp. susceptible to the quality of pixel information obtained from digital scans of spotted features in the microarray image. We address the statistical computation requirements for optimizing data acquisition and processing of digital scans. We consider the use of median filters to reduce noise levels in images and top-hat filters to correct for trends in background values. We also consider, as alternative estimators of spot intensity, disks of fixed radius, proportions of histograms and k-means clustering, either with or without a square-root intensity transformation and background subtraction. We identify, using combinatoric procedures, optimal filter and estimator parameters, in achieving consistency among the replicates of a gene on each microarray. Our results, using test data from microarrays of HCMV, indicate that a highly effective approach for improving reliability and quality of microarray data is to apply a 21 by 21 top-hat filter, then est. spot intensity as the mean of the largest 20% of pixel values in the target region, after a square-root transformation, and cor. for background, by subtracting the mean of the smallest 70% of pixel values. Fortran90 subroutines implementing these methods are available from the authors, or at http://www.bioss.ac.uk/.apprx.chris. Contact: chris@bioss.ac.uk.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 180 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:228683 CAPLUS
DN 138:363393
TI Summaries of Affymetrix GeneChip probe level data
AU Irizarry, Rafael A.; Bolstad, Benjamin M.; Collin, Francois; Cope, Leslie M.; Hobbs, Bridget; Speed, Terence P.
CS Department of Biostatistics, Johns Hopkins University, Baltimore, MD, 21205, USA
SO Nucleic Acids Research (2003), 31(4), e15/1-e15/8 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB High d. oligonucleotide array technol. is widely used in many areas of biomedical research for quant. and highly parallel measurements of gene expression. Affymetrix GeneChip arrays are the most popular. In this technol. each gene is typically represented by a set of 11-20 pairs of probes. In order to obtain expression measures it is necessary to summarize the probe level data. Using two extensive spike-in studies and a diln. study, we developed a set of tools for assessing the effectiveness of expression measures. We found that the performance of the current version of the default expression measure provided by Affymetrix Microarray Suite can be significantly improved by the use of probe level summaries derived from empirically motivated statistical models. In particular, improvements in the ability to detect differentially expressed genes are demonstrated.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 181 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:228413 CAPLUS
DN 138:363391
TI Comparisons and validation of statistical clustering techniques for microarray gene expression data
AU Datta, Susmita; Datta, Somnath
CS Department of Mathematics and Statistics and Department of Biology, Georgia State University, Atlanta, GA, 30303, USA
SO Bioinformatics (2003), 19(4), 459-466 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB With the advent of microarray chip technol., large data sets are emerging contg. the simultaneous expression levels of thousands of genes at various time points during a biol. process. Biologists are attempting to group genes based on the temporal pattern of their expression levels. While the use of hierarchical clustering (UPGMA) with correlation distance' has been the most common in the microarray studies, there are many more choices of clustering algorithms in pattern recognition and statistics literature. At the moment there do not seem to be any clear-cut guidelines regarding the choice of a clustering algorithm to be used for grouping genes based on their expression profiles. In this paper, we consider six clustering algorithms (of various flavors!) and evaluate their performances on a well-known publicly available ***microarray*** data set on sporulation of budding yeast and on two ***simulated*** data sets. Among other things, we formulate three reasonable validation strategies that can be used with any clustering algorithm when temporal observations or replications are present. We evaluate each of these six clustering methods with these validation measures. While the best' method is dependent on the exact validation strategy and the no. of clusters to be used, overall Diana appears to be a solid performer. Interestingly, the performance of correlation-based hierarchical clustering and model-based clustering (another method that has been advocated by a no. of researchers) appear to be on opposite extremes, depending on what validation measure one employs. Next it is shown that the group means produced by Diana are the closest and those produced by UPGMA are the farthest from a model profile based on a set of hand-picked genes.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 182 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:228396 CAPLUS
DN 138:363386
TI A multivariate approach applied to microarray data for identification of genes with cell cycle-coupled transcription
AU Johansson, Daniel; Lindgren, Petter; Berglund, Anders
CS Department of Chemistry, Organic Chemistry, Research group for Chemometrics, Umea University, Swed.
SO Bioinformatics (2003), 19(4), 467-473 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB We have analyzed microarray data using a modeling approach based on the multivariate statistical method partial least squares (PLS) regression to identify genes with periodic fluctuations in expression levels coupled to the cell cycle in the budding yeast, Saccharomyces cerevisiae. PLS has major advantages for analyzing microarray data since it can model data sets with large nos. of variables and with few observations. A response model was derived describing the expression profile over time expected for periodically transcribed genes, and was used to identify budding yeast transcripts with similar profiles. PLS was then used to interpret the importance of the variables (genes) for the model, yielding a ranking list of how well the genes fitted

the generated model. Application of an appropriate cutoff value, calcd. from randomized data, allows the identification of genes whose expression appears to be synchronized with cell cycling. Our approach also provides information about the stage in the cell cycle where their transcription peaks. Three synchronized yeast cell microarray data sets were analyzed, both sep. and combined. Cell cycle-coupled periodicity was suggested for 455 of the 6,178 transcripts monitored in the combined data set, at a significance level of 0.5%. Among the candidates, 85% of the known periodic transcripts were included. Anal. of the three data sets sep. yielded similar ranking lists, showing that the method is robust.
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 183 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:228355 CAPLUS
DN 138:379915
TI Identifying differentially expressed genes using false discovery rate controlling procedures
AU Reiner, Anat; Yekutieli, Daniel; Benjamini, Yoav
CS The Sackler Faculty of Exact Sciences, Department of Statistics and Operations Research, Tel-Aviv University, Tel-Aviv, 69978, Israel
SO Bioinformatics (2003), 19(3), 368-375 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Motivation: DNA microarrays have recently been used for the purpose of monitoring expression levels of thousands of genes simultaneously and identifying those genes that are differentially expressed. The probability that a false identification (type I error) is committed can increase sharply when the no. of tested genes gets large. Correlation between the test statistics attributed to gene co-regulation and dependency in the measurement errors of the gene expression levels further complicates the problem. In this paper the authors address this very large multiplicity problem by adopting the false discovery rate (FDR) controlling approach. To address the dependency problem, the authors present three resampling-based FDR controlling procedures, that account for the test statistics distribution, and compare their performance to that of the naive application of the linear step-up procedure in Benjamini and Hochberg (1995). The procedures are studied using ***simulated*** ***microarray*** data, and their performance is examd. relative to their ease of implementation. Results: Comparative simulation anal. shows that all four FDR controlling procedures control the FDR at the desired level, and retain substantially more power then the family-wise error rate controlling procedures. In terms of power, using resampling of the marginal distribution of each test statistics substantially improves the performance over the naive one. The highest power is achieved, at the expense of a more sophisticated algorithm, by the resampling-based procedures that resample the joint distribution of the test statistics and est. the level of FDR control. Availability: An R program that adjusts p-values using FDR controlling procedures is freely available over the Internet at www.math.tau.ac.il/.apprx.ybenja.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 184 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:221070 CAPLUS
DN 138:363269
TI Open source software for the analysis of microarray data
AU Dudoit, Sandrine; Gentleman, Robert C.; Quackenbush, John
CS University of California, Berkeley, CA, USA
SO BioTechniques (2003), (Suppl.), 45-51 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal; General Review
LA English
AB A review, with refs. DNA microarray assays represent the first widely used application that attempts to build upon the information provided by genome projects in the study of biol. questions. One of the greatest challenges with working with microarrays is collecting, managing, and analyzing data. Although several com. and noncommercial solns. exist, there is a growing body of freely available, open source software that allows users to analyze data using a host of existing techniques and to develop their own and integrate them within the system. Here we review three of the most widely used and comprehensive systems, the statistical anal. tools written in R through the Bioconductor project (http://www.bioconductor.org), the Java-based TM4 software system available from The Institute for Genomic Research (http://www.tigr.org/software), and BASE, the Web-based system developed at Lund University (http://base.thep.lu.se).
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 185 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:221068 CAPLUS
DN 138:349129
TI Microarray-based cancer diagnosis with artificial neural networks
AU Ringner, Markus; Peterson, Carsten
CS Complex Systems Division, Department of Theoretical Physics, Lund University, Swed.
SO BioTechniques (2003), (Suppl.), 30-32,34-35 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal; General Review
LA English
AB A review, with refs. In recent years, the advent of exptl. methods to probe gene expression profiles of cancer on a genome-wide scale has led to widespread use of supervised machine learning algorithms to characterize these profiles. The main applications of these anal. methods range from assigning functional classes of previously uncharacterized genes to classification and prediction of different cancer tissues. This article surveys the application of machine learning algorithms to classification and diagnosis of cancer based on expression profiles. To exemplify the important issues of the classification procedure, the emphasis of this article is on one such method, namely artificial neural networks. In addn., methods to ext. genes that are important for the performance of a classifier, as well as the influence of sample selection on prediction results are discussed.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 186 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:213457 CAPLUS
DN 139:31710
TI How Well Do We Understand the Clusters Found In Microarray Data?
AU Clare, Amanda; King, Ross D.
CS Department of Computer Science, University of Wales, Aberystwyth, Aberystwyth, SY23 3DB, UK
SO In Silico Biology (2002), 2(4), 511-522 CODEN: ISBIFC; ISSN: 1386-6338
PB IOS Press
DT Journal
LA English
AB We wished to quantify the state-of-the-art of our understanding of clusters in microarray data. To do this we systematically compared the clusters produced on sets of microarray data using a representative set of clustering algorithms (hierarchical, k-means, and a modified version of QT_CLUST) with the annotation schemes MIPS, GeneOntol. and GenProtEC. We assumed that if a cluster reflected known biol. its members would share related ontol. annotations. This assumption is the basis of "guilt-by-assocn." and is commonly used to assign the putative function of proteins. To statistically measure the relationship between cluster and annotation we developed a new predictive discriminatory measure. We found that the clusters found in microarray data do not in general agree with functional annotation classes. Although many statistically significant relationships can be found, the majority of clusters are not related to known biol. (as described in annotation ontologies). This implies that use of guilt-by-assocn. is not supported by annotation ontologies. Depending on the est. of the amt. of noise in the data, our results suggest that bioinformatics has only codified a small proportion of the biol. knowledge required to understand microarray data. The annotated clusters can be found at http://www.aber.ac.uk/compsci/Research/bio/dss/gb a/.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 187 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:209424 CAPLUS
DN 139:377465
TI Incorporation of DNA chip technology to the simulation and validation of flux analysis in yeast diauxic growth
AU Huang, Guewha Steven; Hong, Meng-Yen; Liu, Yung-Chuan
CS Institute of Chinese Pharmaceutical Sciences, China Medical College, Taichung, 404, Taiwan
SO Life Sciences (2003), 72(22), 2525-2531 CODEN: LIFSAK; ISSN: 0024-3205
PB Elsevier Science Inc.
DT Journal
LA English
AB We incorporated gene expression information from cDNA ***microarray*** into flux anal. to ***simulate*** yeast diauxic growth. Expression ratios of both growth phases were applied to assign the split ratio at glyoxylate shunt during simulation, in which the equation was math. unsolvable due to the singularity and artificial split ratios, which were traditionally introduced without biol. evidence. In addn., the directionality of ***microarray*** dataset was used as a further constraint during ***simulation*** . Metabolic fluxes obtained by this modified approach are in general consistent with microarray anal. However, discrepancies occurred when the quantity of fluxes was compared, probably due to the substantial redn. of substrates at phase II in which the increase in the enzymic levels was not proportional to the increase of substrate flow, as would be predicted from microarray dataset. The modified flux anal. might have brought a new approach to investigate other cellular pathways.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 188 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:206198 CAPLUS
DN 140:1210
TI Photonic modeling of DNA chips
AU Getin, Stephane
CS Direction de la recherche technologique, CEA centre de Grenoble, Fr.
SO Clefs CEA (2002), Volume Date 2002-2003, 47, 77-79 CODEN: CEACES; ISSN: 0298-6248
PB Commissariat a l'Energie Atomique
DT Journal
LA French
AB Methods of modeling the patterns of distribution of emissions from fluorescent reporter groups in biochips are developed. The spatial distribution of fluorescence emissions from an element on a hybridization microarray is not necessarily uniform. Modeling of the emission patterns can be used to optimize scanning and uniformity of data collection and avoid artifacts in anal.

L6 ANSWER 189 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:206197 CAPLUS
DN 139:63809

TI Simulation of biological systems
AU Gidrol, Xavier
CS Genopole, Evry, Fr.
SO Clefs CEA (2002), Volume Date 2002-2003, 47, 74-77 CODEN: CEACES; ISSN: 0298-6248
PB Commissariat a l'Energie Atomique
DT Journal; General Review
LA French
AB A review. Presented is the use of DNA microarray technol. and gene expression profiling, in conjunction with modeling of biol. systems for evaluation of macromol. function and cellular response to disease status, such as cancer.

L6 ANSWER 190 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:197017 CAPLUS
DN 138:164190
TI Design and implementation of microarray gene expression markup language (MAGE-ML)
AU Spellman, Paul T.; Miller, Michael; Stewart, Jason; Troup, Charles; Sarkans, Ugis; Chervitz, Steve; Bernhart, Derek; Sherlock, Gavin; Ball, Catherine; Lepage, Marc; Swiatek, Marcin; Marks, W. L.; Goncalves, Jason; Markel, Scott; Iordan, Daniel; Shojatalab, Mohammadreza; Pizarro, Angel; White, Joe; Hubley, Robert; Deutsch, Eric; Senger, Martin; Aronow, Bruce J.; Robinson, Alan; Bassett, Doug; Stoeckert, Christian J., Jr.; Brazma, Alvis
CS Department of Cell and Molecular Biology, University of California at Berkeley, Berkeley, CA, 94720-3206, USA
SO GenomeBiology [online computer file] (2002), 3(9), No pp. given CODEN: GNBLFW; ISSN: 1465-6914 URL: http://www.genomebiology.com/content/pdf/gb-2002-3-9-research0046.pdf
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Meaningful exchange of microarray data is currently difficult because it is rare that published data provide sufficient information depth or are even in the same format from one publication to another. Only when data can be easily exchanged will the entire biol. community be able to derive the full benefit from such microarray studies. To this end we have developed three key ingredients towards standardizing the storage and exchange of microarray data. First, we have created a minimal information for the annotation of a microarray expt. (MIAME)-compliant conceptualization of microarray expts. modeled using the unified modeling language (UML) named MAGE-OM (microarray gene expression object model). Second, we have translated MAGE-OM into an XML-based data format, MAGE-ML, to facilitate the exchange of data. Third, some of us are now using MAGE (or its progenitors) in data prodn. settings. Finally, we have developed a freely available software tool kit (MAGE-STK) that eases the integration of MAGE-ML into end user's systems. MAGE will help microarray data producers and users to exchange information by providing a common platform for data exchange, and MAGE-STK will make the adoption of MAGE easier.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 191 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:197015 CAPLUS
DN 138:164077
TI Have microarrays failed to deliver for developmental biology?
AU Livesey, Rick
CS Wellcome Trust/Cancer Research UK Inst. of Cancer, University of Cambridge, Cambridge, CB2 1QR, UK
SO GenomeBiology [online computer file] (2002), 3(9), No pp. given CODEN: GNBLFW; ISSN: 1465-6914 URL: http://www.genomebiology.com/content/pdf/gb-2002-3-9-comment2009.pdf
PB BioMed Central Ltd.
DT Journal; General Review; (online computer file)
LA English
AB A review with 29 refs. Comprehensive microarrays covering large nos. of the predicted expressed transcripts for some invertebrates and vertebrates have been available for some time. Despite predictions that this technol. will transform biol., to date there have been few published studies using microarrays to generate novel insights in developmental biol.
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 192 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:190442 CAPLUS
DN 139:21713
TI CATMA: a complete arabidopsis GST database
AU Crowe, Mark L.; Serizet, Carine; Thareau, Vincent; Aubourg, Sebastien; Rouze, Pierre; Hilson, Pierre; Beynon, Jim; Weisbeek, Peter; van Hummelen, Paul; Reymond, Philippe; Paz-Ares, Javier; Nietfeld, Wilfried; Trick, Martin
CS Laboratoire associe de l'INRA, Fr.
SO Nucleic Acids Research (2003), 31(1), 156-158 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The Complete Arabidopsis Transcriptome Microarray (CATMA) database contains gene sequence tags (GST) and gene model sequences for over 70% of the predicted genes in the Arabidopsis thaliana genome as well as primer sequences for GST amplification and a wide range of supplementary information. All CATMA GST sequences are specific to the gene for which they were designed, and all gene models were predicted from a complete reannotation of the genome using uniform parameters. The database is searchable by sequence name, sequence homol. or direct SQL query.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 193 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:190408 CAPLUS
DN 139:21706
TI The Stanford Microarray Database: data access and quality assessment tools
AU Gollub, Jeremy; Ball, Catherine A.; Binkley, Gail; Demeter, Janos; Finkelstein, David B.; Hebert, Joan M.; Hernandez-Boussard, Tina; Jin, Heng; Kaloper, Miroslava; Matese, John C.; Schroeder, Mark; Brown, Patrick O.; Botstein, David; Sherlock, Gavin
CS Department of Genetics, Center for Clinical Sciences Research, Stanford University, Stanford, CA, 94305-5163, USA
SO Nucleic Acids Research (2003), 31(1), 94-96 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The Stanford Microarray Database (SMD) serves as a microarray research database for Stanford investigators and their collaborators. In addn., SMD functions as a resource for the entire scientific community, by making freely available all of its source code and providing full public access to data published by SMD users, along with many tools to explore and analyze those data. SMD currently provides public access to data from 3,500 microarrays, including data from 85 publications, and this total is increasing rapidly. Some of the SMD's newer tools for accessing public data, assessing data quality and for data anal. are described.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 194 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:190405 CAPLUS
DN 139:21703
TI NetAffx: Affymetrix probesets and annotations
AU Liu, Guoying; Loraine, Ann E.; Shigeta, Ron; Cline, Melissa; Cheng, Jill; Valmeekam, Venu; Sun, Shaw; Kulp, David; Siani-Rose, Michael A.
CS Department of Bioinformatics, Affymetrix, Inc, Emeryville, CA, 94608, USA
SO Nucleic Acids Research (2003), 31(1), 82-86 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB NetAffx details and annotates probesets on Affymetrix GeneChip microarrays. These annotations include: static information specific to the probeset compn.; sequence annotations extd. from public databases; and protein sequence-level annotations derived from public domain programs as well as libraries of hidden Markov models (HMMs) developed by Affymetrix. For each probeset, NetaAffx lists the probe sequences, and the consensus sequence interrogated by the probes; for the larger chip sets, interactive maps display this sequence data in genomic context. Sequence annotations include gene ontol. (GO) terms and depiction of GO graph relationships; predicted protein domains and motifs; orthologous sequences; links to relevant pathways; and links to public databases including UniGene, LocusLink, SWISS-PROT and OMIM.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 195 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:190401 CAPLUS
DN 138:266321
TI ArrayExpress-a public repository for microarray gene expression data at the EBI
AU Brazma, Alvis; Parkinson, Helen; Sarkans, Ugis; Shojatalab, Mohammadreza; Vilo, Jaak; Abeygunawardena, Niran; Holloway, Ele; Kapushesky, Misha; Kemmeren, Patrick; Lara, Gonzalo Garcia; Oezcimen, Ahmet; Rocca-Serra, Philippe; Sansone, Susanna-Assunta
CS European Bioinformatics Institute, EMBL-EBI, Hinxton, CB10 1SD, UK
SO Nucleic Acids Research (2003), 31(1), 68-71 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB ArrayExpress is a new public database of microarray gene expression data at the EBI, which is a generic gene expression database designed to hold data from all microarray platforms. ArrayExpress uses the annotation std. Min. Information About a Microarray Expt. (MIAME) and the assocd. XML data exchange format Microarray Gene Expression Markup Language (MAGE-ML) and it is designed to store well annotated data in a structured way. The ArrayExpress infrastructure consists of the database itself, data submissions in MAGE-ML format or via an online submission tool MIAMExpress, online database query interface, and the Expression Profiler online anal. tool. ArrayExpress accepts three types of submission, arrays, expts. and protocols, each of these is assigned an accession no. Help on data submission and annotation is provided by the curation team. The database can be queried on parameters such as author, lab., organism, expt. or array types. With an increasing no. of organisations adopting MAGE-ML std., the vol. of submissions to ArrayExpress is increasing rapidly. The database can be accessed at http://www.ebi.ac.uk/arrayexpres s.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 196 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:174195 CAPLUS
DN 138:201290
TI High throughput screening micro array platform
IN Luo, Shun

PA USA
SO U.S. Pat. Appl. Publ., 12 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE ---------
------ ---- -------- ---------- --------
PI US 2003044320 A1 20030306 US 2001-943937 20010831 US 2003044808 A1 20030306 US 2001-20025 20011207 WO 2003018772 A2 20030306 WO 2002-US27971 20020903 WO 2003018772 A3 20030417 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2001-943937 A2 20010831
AB The present invention discloses platform technol. which integrates current DNA micro array technol. and current high throughput screening technol. The invention contains three major components: an array gridding head, the hybrid glass chip/micro titer plate format plate that contains the micro arrays produced by the arraying/gridding head, and an array scanner with data acquisition and anal. software. The arraying/gridding head is capable of simultaneously depositing DNA, RNA peptidalnucleic acid (PNA), or polypeptide (protein) solns., etc. onto chem. treated modified surfaces in 96, 384 and 1536 well formats of repeating patterns on the modified glass chips/plates. The micro arrays are composed of arrays of 96, 384 or 1536 patterns with defined specifications on the single glass "chip" packaged as a std. micro titer plate conforming to the Society of Biomol. Screening (SBS) specification for robotic handling. The array reading and anal. component includes an array scanning device and anal. software. The array scanner is configured to read micro arrays in the micro titer plate format of the invention as well as current microscope slide format. Thus, the invention transforms current DNA micro array technol. into a high throughput screening tool.

L6 ANSWER 197 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:164000 CAPLUS
DN 138:332849
TI MAPPFinder: using Gene Ontology and GenMAPP to create a global gene-expression profile from microarray data
AU Doniger, Scott W.; Salomonis, Nathan; Dahlquist, Kam D.; Vranizan, Karen; Lawlor, Steven C.; Conklin, Bruce R.
CS Gladstone Institute of Cardiovascular Disease, University of California, San Francisco, CA, 94141-9100, USA
SO GenomeBiology (2002), 4(1), No pp. given CODEN: GNBLFW; ISSN: 1465-6914 URL: http://genomebiology.com/content/pdf/gb-2003-4-1-r7.pdf
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB MAPPFinder is a tool that creates a global gene-expression profile across all areas of biol. by integrating the annotations of the Gene Ontol. (GO) Project with the free software package GenMAPP (http://www.GenMAPP.org). The results are displayed in a searchable browser, allowing the user to rapidly identify GO terms with over-represented nos. of gene expression changes. Clicking on GO terms generates GenMAPP graphical files where gene relationships can be explored, annotated, and files can be freely exchanged.
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 198 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:152440 CAPLUS
DN 138:169559
TI Computer-based support system for DNA sequence analysis
IN Higuchi, Chihiro; Aoki, Mikio
PA Sumitomo Pharmaceuticals Co., Ltd., Japan
SO Jpn. Kokai Tokkyo Koho, 9 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------
------ ---- -------- ---------- --------
PI JP 2003058548 A2 20030228 JP 2001-250276 20010821
PRAI JP 2001-250276 20010821
AB The invention relates to a computer-based system for supporting DNA sequence anal. Data obtained from a homol. search carried out with DNA chips or protein chips are complied in databases. A search using individual probe sequences are carried out against this secondary database. The system includes software and worldwide web internet server.

L6 ANSWER 199 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:150248 CAPLUS
DN 138:183451
TI Microarray processing apparatus for substance to be processed
IN Takei, Shigeo; Tanaka, Osamu; Miyamoto, Yoshiaki
PA Aloka Co., Ltd., Japan
SO Jpn. Kokai Tokkyo Koho, 21 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------
------ ---- -------- ---------- --------
PI JP 2003057255 A2 20030226 JP 2001-241222 20010808
PRAI JP 2001-241222 20010808
AB A microarray processing app. for a substance to be processed (e.g., nucleic acid) is provided, with which the operation for processing a substance to be processed is easy, and the labor and time required for the operation is reduced. The processing app. for a substance to be processed (microarray processing app.) comprises an app. main body equipped with two sealable processing tanks (reaction tanks), a personal computer, and four processing units in total accommodated in the resp. processing tank in such a way that they are freely mounted or detached. The app. main body is equipped with a horizontal stage and a vertical stage. On the horizontal stage, installed are a chip-mounting part, a probe soln.-accommodating container-mounting part, a container-mounting part, and the resp. processing tank. On the vertical stage, installed is a probe soln.-supplying means (reaction liq.-supplying means). In addn., a supply circuit, a discharge circuit, and a temp.-regulating means are mainly installed inside the app. main body. Diagrams describing the app. assembly are given.

L6 ANSWER 200 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:148135 CAPLUS
DN 138:183449
TI Microarray processing apparatus for substance to be processed
IN Miyamoto, Yoshiaki; Takei, Shigeo; Tanaka, Osamu
PA Aloka Co., Ltd., Japan
SO Jpn. Kokai Tokkyo Koho, 21 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------
------ ---- -------- ---------- --------
PI JP 2003057254 A2 20030226 JP 2001-241220 20010808
PRAI JP 2001-241220 20010808
AB A microarray processing app. for a substance to be processed (e.g., nucleic acid) is provided, with which the operation for processing a substance to be processed is easy, and the labor and time required for the operation is reduced. The processing app. for a substance to be processed (microarray processing app.) comprises an app. main body equipped with two sealable processing tanks (reaction tanks), a personal computer, and four processing units in total accommodated in the resp. processing tank in such a way that they are freely mounted or detached. The app. main body is equipped with a horizontal stage and a vertical stage. On the horizontal stage, installed are a chip-mounting part, a probe soln.-accommodating container-mounting part, a container-mounting part, and the resp. processing tank. On the vertical stage, installed is a probe soln.-supplying means (reaction liq.-supplying means). In addn., a supply circuit, a discharge circuit, and a temp.-regulating means are mainly installed inside the app. main body. Diagrams describing the app. assembly are given.

L6 ANSWER 201 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:148134 CAPLUS
DN 138:183448
TI Microarray processing apparatus for substance to be processed
IN Takei, Shigeo; Miyamoto, Yoshiaki; Tanaka, Osamu
PA Aloka Co., Ltd., Japan
SO Jpn. Kokai Tokkyo Koho, 28 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------
------ ---- -------- ---------- --------
PI JP 2003057247 A2 20030226 JP 2001-244936 20010810
PRAI JP 2001-244936 20010810
AB A microarray processing app. for a substance to be processed (e.g., nucleic acid) is provided, with which the operation for processing a substance to be processed is easy, and the labor and time required for the operation is reduced. The processing app. for a substance to be processed (microarray processing app.) comprises an app. main body equipped with two sealable processing tanks (reaction tanks), a personal computer, and four processing units in total accommodated in the resp. processing tank in such a way that they are freely mounted or detached. The app. main body is equipped with a horizontal stage and a vertical stage. On the horizontal stage, installed are a chip-mounting part, a probe soln.-accommodating container-mounting part, a container-mounting part, and the resp. processing tank. On the vertical stage, installed is a probe soln.-supplying means (reaction liq.-supplying means). In addn., a supply circuit, a discharge circuit, and a temp.-regulating means are mainly installed inside the app. main body. Diagrams describing the app. assembly are given.

L6 ANSWER 202 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:146691 CAPLUS
DN 138:183446
TI Microarray processing apparatus for substance to be processed
IN Tanaka, Osamu; Takei, Shigeo; Miyamoto, Yoshiaki
PA Aloka Co., Ltd., Japan
SO Jpn. Kokai Tokkyo Koho, 21 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------
------ ---- -------- ---------- --------
PI JP 2003057250 A2 20030226 JP 2001-241221 20010808
PRAI JP 2001-241221 20010808
AB A microarray processing app. for a substance to be processed (e.g., nucleic acid) is provided, with which the operation for processing a substance to be processed is easy, and the labor and time required for the operation is reduced. The processing app. for a substance to be processed (microarray processing app.) comprises an app.

main body equipped with two sealable processing tanks (reaction tanks), a personal computer, and four processing units in total accommodated in the resp. processing tank in such a way that they are freely mounted or detached. The app. main body is equipped with a horizontal stage and a vertical stage. On the horizontal stage, installed are a chip-mounting part, a probe soln.-accommodating container-mounting part, a container-mounting part, and the resp. processing tank. On the vertical stage, installed is a probe soln.-supplying means (reaction liq.-supplying means). In addn., a supply circuit, a discharge circuit, and a temp.-regulating means are mainly installed inside the app. main body. Diagrams describing the app. assembly are given.

L6 ANSWER 203 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:135981 CAPLUS
DN 138:327113
TI Numerical simulation of the stamping process through microchannels
AU Lin, Shih-Chang; Tseng, Fangang; Chieng, Ching-Chang
CS Department of Engineering and System Science, National Tsing Hua University, Hsinchu, Taiwan, 30043, Peop. Rep. China
SO Journal of Colloid and Interface Science (2003), 258(1), 179-185 CODEN: JCISA5; ISSN: 0021-9797
PB Elsevier Science
DT Journal
LA English
AB This study proposes a stamper array chip with embedded microchannels that delivers fixed size and shape liq. samples to a bottom chip for quant. biodiagnosis and bioassays. The transfer process and physics are analyzed by solving first-principle equations numerically. The simulation proves that the surface tension force inside a microchannel plays an important role in driving the liq. fluid from the reservoir to the tip of the microchannel and causes some degree of liq.-air interface oscillation due to the interaction of a pressure wave and the surface tension force. The oscillation of the meniscus-free surface helps the delivery of the liq. to the bottom chip by forming microchannels and attaching to the surface. Most of all, the simulation of the stamping process indicates that the control of spot size transferred to the bottom surface is feasible for precise diagnosis under different stamping speeds and/or various contact angles due to different surface tension coeffs. between fluids and solid surfaces.
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 204 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:134180 CAPLUS
DN 139:36009
TI TM4: A free, open-source system for microarray data management and analysis
AU Saeed, A. I.; Sharov, V.; White, J.; Li, J.; Liang, W.; Bhagabati, N.; Braisted, J.; Klapa, M.; Currier, T.; Thiagarajan, M.; Sturn, A.; Snuffin, M.; Rezantsev, A.; Popov, D.; Ryltsov, A.; Kostukovich, E.; Borisovsky, I.; Liu, Z.; Vinsavich, A.; Trush, V.; Quackenbush, J.
CS The Institute for Genomic Research, Rockville, MD, USA
SO BioTechniques (2003), 34(2), 374-376,378 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
AB Microarrays have emerged as the premier tool for studying gene expression on a genomic scale. Scientists seeking to harness the potential of this technique are often challenged by the large quantities of data produced. In support of their ongoing work in microarray anal. of gene expression, the authors developed a suite of software that allow users in the lab. to capture, manage, and analyze effectively data from DNA microarray expts. The TM4 suite of tools consist of four major applications: Microarray Data Manager (MADAM), TIGR_Spotfinder, Microarray Data Anal. System (MIDAS), and Multiexperiment Viewer (MeV), as well as a Minimal Information About a Microarray Expt. (MIAME)-compliant MySQL database. The TM4 software system represents a comprehensive, extensible, open-source, and freely available collection of tools that will be of use to a wide range of labs. conducting microarray expts.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 205 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:133859 CAPLUS
DN 138:148667
TI Methods for signal generation and amplification of target nucleic acids in arrays
IN Gellibolian, Robert
PA USA
SO U.S. Pat. Appl. Publ., 26 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2003036065 A1 20030220 US 2001-932728 20010817
PRAI US 2001-932728 20010817
AB A method and system for signal generation and signal amplification from an array contg. bound, unlabeled target mols. Following exposure of the array to a sample soln. contg. unlabeled target RNA mols., blunt ends are generated on each probe/target double-stranded hybrid labeled primer oligonucleotide linker is then bound to the blunt ends. Next, in an iterative, inner process, addnl. layers of labeled oligonucleotide, linkers are added, shell-by-shell, to form a dendrimer-like mol. complex bound through the oligonucleotide linker to the probe/target hybrid.

L6 ANSWER 206 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:132730 CAPLUS
DN 138:148664
TI Apparatus and computer program for processing of biological samples
IN Shibuya, Satoshi; Kaneko, Yasuo; Suzuki, Hiroyuki; Machida, Kazuhisa; Takano, Masaki
PA Hitachi Ltd., Japan
SO Jpn. Kokai Tokkyo Koho, 31 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI JP 2003050242 A2 20030221 JP 2001-240152 20010808
PRAI JP 2001-240152 20010808
AB The app. has a unit for multistep-processing of a plurality of samples and a recording unit contg. memory devices which store the information of the biol. samples, the information of the process steps, and the information of the results of processing. The app. and computer program are useful for pretreatment including extn., amplification by PCR, diln., and modification of nucleic acids, etc., before electrophoresis. Diagrams of the app. and flowcharts for PCR-SSCP (single-strand conformation polymorphism) and gene anal. are given.

L6 ANSWER 207 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:129887 CAPLUS
DN 138:315337
TI Surface electrostatic effects in oligonucleotide microarrays: Control and optimization of binding thermodynamics
AU Vainrub, Arnold; Pettitt, B. Montgomery
CS Department of Chemistry, University of Houston, Houston, TX, 77204-5003, USA
SO Biopolymers (2003), 68(2), 265-270 CODEN: BIPMAA; ISSN: 0006-3525
PB John Wiley & Sons, Inc.
DT Journal
LA English
AB We present a theor. thermodn. framework for the design of more efficient oligonucleotide microarrays. A general thermodn. relation is derived to describe the electrostatic surface effects on the binding of the assayed biomol. to a surface-tethered mol. probe. The relation is applied to analyze how the nucleic acid target, the oligonucleotide probe, and their DNA duplex electrostatic interactions with the surface affect the hybridization on DNA arrays. Taking advantage of a closed form exact soln. of the linear Poisson-Boltzmann equation for a charged ion-penetrable sphere in electrolyte soln. interacting with a plane wall, we study the effects of the surface and soln. conditions. Binding free energy is found as a function of the surface material, dielec. or metal, the surface charge d., linker mol. length, temp., and added salt content. The charge or elec. potential of the dielec. or metal surface, resp., is shown to dominate the hybridization, esp. at low added salt or short linker length. We predict that substantial enhancement of sensitivity, selectivity, and reliability of microarrays can be achieved by control of the surface conditions. As examples, we discuss how to overcome two limitations of current technologies: nonequal sensitivity of the probes with different GC and AT bases content, and poor match/mismatch discrimination. In addn., we suggest the design of microarray conditions where the tested nucleic acid is unfolded, thus making possible the screening of a larger sequence with single nucleotide resoln. These promising findings are discussed and further exptl. tests suggested.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 208 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:128284 CAPLUS
DN 138:302568
TI Analysis of B cell memory formation using DNA microarrays
AU Vinuesa, Carola G.; Cook, Matthew C.; Cooke, Michael P.; Maclennan, Ian C. M.; Goodnow, Christopher C.
CS Medical Genome Centre, John Curtin School of Medical Research, Australian National University, ACT, Australia
SO Annals of the New York Academy of Sciences (2002), 975(Microarrays, Immune Responses, and Vaccines), 33-45 CODEN: ANYAA9; ISSN: 0077-8923
PB New York Academy of Sciences
DT Journal
LA English
AB DNA microarray anal. of B cell subsets has identified comprehensive programs of gene expression that distinguish B cells at discrete stages of differentiation. The next task is to identify key genetic signals within these complex programs that regulate the dynamic cellular events during B cell activation in vivo. After stimulation with antigen, naive B cells proliferate and differentiate, and then produce antibodies. Crucial qual. differences in antibody responses are obsd. depending on whether or not B cells receive T cell help during activation. Proteins, lipopolysaccharides, and polysaccharides stimulate T-dependent (TD), T-independent type 1 (TI-1), and type 2 (TI-2) antibody responses, resp. Only TD responses generate somatically mutated antibody-forming (plasma) cells and memory B cells, which produce high affinity anamnestic responses to subsequent antigen challenge. Somatic mutation of Ig genes occurs during B cell proliferation in germinal centers (GC), which are typical in TD responses but rare in TI responses. However, we have described a model, which is exceptional because numerous large GC form in response to a model TI-2 antigen, (4-hydroxy-3-nitrophenyl) acetyl (NP)-Ficoll. Significantly, these GC undergo involution before memory B cells are generated. This model provides an opportunity to investigate the genetic signals that drive memory cell formation, and we have compared global gene expression in TI and TD GC to identify a relatively small no. of genes that are differentially expressed between the two prototypic B cell responses. This model demonstrates how genome-scale technol. can be adapted to investigate specific aspects of B cell biol.
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 209 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:123908 CAPLUS
DN 138:298774
TI Pattern recognition techniques in microarray data analysis: A survey
AU Valafar, Faramarz
CS Department of Computer Science, San Diego State University, San Diego, CA, 92182, USA
SO Annals of the New York Academy of Sciences (2002), 980(Techniques in Bioinformatics and Medical Informatics), 41-64 CODEN: ANYAA9; ISSN: 0077-8923
PB New York Academy of Sciences
DT Journal
LA English
AB Recent development of technologies (e.g., microarray technol.) that are capable of producing massive amts. of genetic data has highlighted the need for new pattern recognition techniques that can mine and discover biol. meaningful knowledge in large data sets. Many researchers have begun an endeavor in this direction to devise such data-mining techniques. As such, there is a need for survey articles that periodically review and summarize the work that has been done in the area. This article presents one such survey. The first portion of the paper is meant to provide the basic biol. (mostly for non-biologists) that is required in such a project. This part is only meant to be a starting point for those experts in the tech. fields who wish to embark on this new area of bioinformatics. The second portion of the paper is a survey of various data-mining techniques that have been used in mining microarray data for biol. knowledge and information (such as sequence information). This survey is not meant to be treated as complete in any form, since the area is currently one of the most active, and the body of research is very large. Furthermore, the applications of the techniques mentioned here are not meant to be taken as the most significant applications of the techniques, but simply as examples among many.
RE.CNT 95 THERE ARE 95 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 210 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:102814 CAPLUS
DN 138:234200
TI Prediction of feature spread for microarray printing using protein and DNA solutions
AU Smith, Jason T.; Reichert, W. Monty
CS Department of Biomedical Engineering, Duke University, Durham, NC, 27708, USA
SO Langmuir (2003), 19(7), 3078-3080 CODEN: LANGD5; ISSN: 0743-7463
PB American Chemical Society
DT Journal
LA English
AB The following study outlines the results of printing expts. conducted with a variety of DNA and protein samples for the optimization of microarray d. and the correlation of feature size with the predictive model.
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 211 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:90887 CAPLUS
DN 138:281831
TI How many genes are needed for a discriminant microarray data analysis
AU Li, Wentian; Yang, Yaning
CS Laboratory of Statistical Genetics, The Rockefeller University, New York, NY, 10021, USA
SO Methods of Microarray Data Analysis, Papers from CAMDA '00, Durham, NC, United States, Dec. 18-19, 2000 (2002), Meeting Date 2000, 137-149. Editor(s): Lin, Simon M.; Johnson, Kimberly F. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69DOO6; ISBN: 0-7923-7564-5
DT Conference
LA English
AB The anal. of the leukemia data from Whitehead/MIT group is a discriminant anal. (also called a supervised learning). Among thousands of genes whose expression levels are measured, not all are needed for discriminant anal. A gene may either not contribute to the sepn. of two types of tissues/cancers, or it may be redundant because it is highly correlated with other genes. There are two theor. frameworks in which variable selection (or gene selection in our case) can be addressed. The first is model selection, and the second is model averaging. We have carried out model selection using Akaike information criterion and Bayesian information criterion with logistic regression (discrimination, prediction, or classification) to det. the no. of genes that provide the best model. These model selection criteria set upper limits of 22.apprx.25 and 12.apprx.13 genes for this data set with 38 samples, and the best model consists of only one (no.4847, zyxin) or two genes. We have also carried out model averaging over the best single-gene logistic predictors using three different wts.: maximized likelihood, prediction rate on training set, and equal wt. We have obsd. that the performance of most of these weighted predictors on the testing set is gradually reduced as more genes are included, but a clear cutoff that separates good and bad prediction performance is not found.
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 212 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:90882 CAPLUS
DN 138:315294
TI A method to improve detection of disease using selectively expressed genes in microarray data
AU Aris, Virginie; Recce, Michael
CS Center for Applied Genomics, Public Health Research Institute, and Cent. for Computational Biol. and Bioeng., NJIT, USA
SO Methods of Microarray Data Analysis, Papers from CAMDA '00, Durham, NC, United States, Dec. 18-19, 2000 (2002), Meeting Date 2000, 69-80. Editor(s): Lin, Simon M.; Johnson, Kimberly F. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69DOO6; ISBN: 0-7923-7564-5
DT Conference
LA English
AB We describe a method to improve the classification of microarray data presented in Golub et al. (1999) through the anal. of present vs. absent calls in selectively expressed genes. This method does not rely on scaling or normalization factors in the comparison of data across subjects. Several genes in the Golub et al. (1999) dataset are selectively expressed between acute myeloid leukemia (AML) and acute lymphoblastic leukemia (ALL). We show that the presence or absence of expression in the 30 to 100 most selective genes is sufficient to correctly classify and diagnose the disease state of the subjects in the training dataset, and to with only one error in the independent set. In this initial anal., the level of gene expression is not used. The exemplar, or cluster center, for each of the two diseases is computed as the real-valued av. of the (expressed/not expressed) binary values for each of the most selective genes of the subjects with each disease (27 ALL, 11 AML). The Euclidean distance to each of the two exemplars is then computed for each subject. Members of a cluster are closer (smaller in distance) to the exemplar of that cluster than to the exemplar of another. For example, the range of distances of the 10 most selective genes from the AML subjects in the training set to the AML exemplar is 0.05 to 0.28, and to the ALL exemplar is 0.62 to 0.87. These data, along with the distances of the ALL subjects from the two exemplars show that the two clusters are well sepd., with no overlap.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 213 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:90879 CAPLUS
DN 138:315126
TI Evolutionary computation in microarray data analysis
AU Moore, Jason H.; Parker, Joel S.
CS Program in Human Genetics, Department of Molecular Physiology and Biophysics, Vanderbilt University Medical School, Nashville, TN, 37232-0700, USA
SO Methods of Microarray Data Analysis, Papers from CAMDA '00, Durham, NC, United States, Dec. 18-19, 2000 (2002), Meeting Date 2000, 23-35. Editor(s): Lin, Simon M.; Johnson, Kimberly F. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69DOO6; ISBN: 0-7923-7564-5
DT Conference; General Review
LA English
AB A review with refs. We are facing an information explosion in the biomedical sciences. For example, our ability to measure the expression levels of thousands of different genes simultaneously in a particular cell or tissue has far outpaced our ability to store, manage, and analyze the data being generated. In this review, we explore the use of evolutionary computation for dealing with some of the difficult statistical and computational challenges that have resulted from the development and implementation of new technologies such as DNA microarrays. We review genetic algorithms and genetic programming as evolutionary computation strategies that have been applied to the anal. of DNA microarray data.
RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 214 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:90878 CAPLUS
DN 139:133026
TI Data mining and machine learning methods for microarray analysis
AU Dubitzky, Werner; Granzow, Martin; Berrar, Daniel
CS Intelligent Bioinformatics Systems Group, German Cancer Research Center, Heidelberg, Germany
SO Methods of Microarray Data Analysis, Papers from CAMDA '00, Durham, NC, United States, Dec. 18-19, 2000 (2002), Meeting Date 2000, 5-22. Editor(s): Lin, Simon M.; Johnson, Kimberly F. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69DOO6; ISBN: 0-7923-7564-5
DT Conference
LA English
AB Microarray expts. provide the scientific community with huge amts. of data. Without appropriate methodologies and tools, significant information and knowledge hidden in these data may not be discovered. Therefore, there is a need for methods capable of handling and exploring large data sets. The field of data mining and machine learning provides a wealth of methodologies and tools for analyzing large data sets. Two classical machine learning techniques suitable for microarray anal. are described, namely decision trees and artificial neural networks. An outline of how these approaches can be used into a wider data mining framework is presented.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 215 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:77606 CAPLUS
DN 138:132256
TI Method and computer software to computer-design optimum oligo-probe from nucleic acid base sequences analyzed for DNA chip
IN Aoki, Yoshiaki; Ishikawa, Mitsuyoshi
PA Japan
SO U.S. Pat. Appl. Publ., 21 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE ---------
------ ---- -------- ---------- --------

PI US 2003023419 A1 20030130 US 2002-176293 20020620 JP 2003125772 A2 20030507 JP 2002-173467 20020613 JP 2003099438 A2 20030404 JP 2002-180593 20020620
PRAI JP 2001-225181 A 20010620
AB The invention related to a computer software program to design an optimum oligo-nucleic acid base sequence candidate from nucleic acid base sequences being analyzed using a computer for DNA chip. The program comprises a first command to receive the specification of resp. tolerated ranges of double-chain bond temp., base sequence length and GC content, and to store the information on the priority order of resp. items in the memory. The program comprises a second command, while extending the partial sequence in the aforementioned nucleic acid base sequences being analyzed, to det. whether or not a sequence in each length falls within resp. tolerated ranges based on the priority items received by the aforementioned first command, and if it does fall within the ranges, to output the partial sequence in the applicable length as an oligo-nucleic acid base sequence candidate. The program comprises a third command to display, based on the aforementioned priority order, the oligo-nucleic acid sequence candidate outputted by the aforementioned second command along with the values of resp. items.

L6 ANSWER 216 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:74584 CAPLUS
DN 138:118067
TI Introduction to the practical analysis of DNA microarray data
AU Bono, Hidemasa; Nakao, Mitsuteru C.
CS Yokohama Res. Lab., RIKEN, Japan
SO Tanpakushitsu Kakusan Koso (2003), 48(2), 167-172 CODEN: TAKKAJ; ISSN: 0039-9450
PB Kyoritsu Shuppan
DT Journal; General Review
LA Japanese
AB A review on the tools for the data preprocessing and mining in DNA microarray and DNA chip anal.; cluster anal. of gene expression by Cluster/TreeView, MeV, and R; and a search tool for genes with similarities in expression profiles. READ (RIKEN expression array database; expression profile data from the RIKEN mouse cDNA microarray) and RINGENE (READ integrates gene expression neighbor) are briefly introduced.

L6 ANSWER 217 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:74478 CAPLUS
DN 138:281790
TI Improved analytical methods for microarray-based genome-composition analysis
AU Kim, Charles C.; Joyce, Elizabeth A.; Chan, Kaman; Falkow, Stanley
CS Dept. of Microbiology and Immunology, Stanford Univ. Med. Center, Stanford, CA, 94305, USA
SO GenomeBiology (2002), 3(11), No pp. given CODEN: GNBLFW; ISSN: 1465-6914
URL: http://genomebiology.com/2002/3/11/research/0065.1
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Background: Whereas genome sequencing has given the authors' high-resoln. pictures of many different species of bacteria, microarrays provide a means of obtaining information on genome compn. for many strains of a given species. Genome-compn. anal. using microarrays, or "genomotyping", can be used to categorize genes into "present" and "divergent" categories based on the level of hybridization signal. This typically involves selecting a signal values that is used as a cutoff to discriminate present (high signal) and divergent (low signal) genes. Current methodol. uses empirical detn. of cutoffs for classification into these categories, but this methodol. is subject to several problems that can result in the misclassification of many genes. Results: the authors describe a method that depends on the shape of the signal-ratio distribution and does not require empirical detn. of a cutoff. Moreover, the cutoff is detd. on an array-to-array basis, accounting for variation in strain compn. and hybridization quality. The algorithm also provides an est. of the probability that any given gene is present, which provides a measure of confidence in the categorical assignment. Conclusions: Many genes previously classified as present using static methods are in fact divergent on the basis of microarray signal; this is cor. by the algorithm. The authors have reassigned hundreds of genes from previous genomotyping studies of Helicobacter pylori and Campylobacter jejuni strains, and expect that the algorithm should be widely applicable to genomotyping data.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 218 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:72885 CAPLUS
DN 138:281786
TI New protocol in spotting microarray technique
AU Iacobas, A. D.; Urban, Marcia; Spray, D. C.
CS Albert Einstein College of Medicine, Bronx, NY, USA
SO Romanian Journal of Physiology (2002), Volume Date 2000, 37(1-4), 69-80
CODEN: RJOPEV; ISSN: 1223-4974
PB Editura Academiei Romane
DT Journal
LA English
AB The "spotting" microarray technique, consisting in large sets of DNA sequences spotted on poly-L-lysine-coated glass microscope slides, has been developed to comparatively analyze genome-wide patterns of mRNA expression. It is now a valuable tool employed in order to quant. monitor gene expression profiles, as well as to analyze the alterations produced in case of genetic diseases, or induced by different treatments, abnormal nutrition and toxin. Our group improved the std. protocol as well as the results spreadsheet, adding new expts. and math. processing procedures in order to increase the accuracy of the data and get new information. In this contribution, we propose and verify two procedures to correct the spot ratios and a new protocol to get the normal variability of the digital gene expression.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 219 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:69098 CAPLUS
DN 138:119565
TI Microarray biochemical analysis system
IN Some, Masato; Eto, Masahiro
PA Fuji Photo Film Co., Ltd., Japan
SO Jpn. Kokai Tokkyo Koho, 8 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI JP 2003028863 A2 20030129 JP 2001-213094 20010713
PRAI JP 2001-213094 20010713
AB A microarray biochem. anal. system with an improved efficiency is provided, with which a visual observation is also realized. The biochem. anal. system comprises a point excitation means for generating an accelerated phosphorescence luminescent light by irradiating an excitation light to a site on an accumulative fluorescent body sheet corresponding to each hole on a membrane, a detection app. for reading the accelerated phosphorescence luminescent light generated at the resp. site and obtaining the numerical value data for each spot, a numerical value data anal. app. for performing an anal. with the numerical value data, a simulated imaging data formation app. for forming the simulated imaging data based on the numerical value data, and a computer equipped with a monitor for displaying the simulated imaging data as an image, and an imaging data anal. software. A flow diagram describing the system assembly is given.

L6 ANSWER 220 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:58686 CAPLUS
DN 138:86089
TI Instruments and methods for creating a tissue microarray
IN Chasse, Stephen V.; Chu, Sunny Wai Keung
PA Ardais Corporation, USA
SO U.S. Pat. Appl. Publ., 12 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2003017446 A1 20030123 US 2002-198593 20020718
PRAI US 2001-306741P P 20010720
AB An instrument for generating a tissue microarray includes a coring tool for coring and removing a sample core from the tissue sample contained in the donor block. An image capture device for capturing a histol. image of a fixed section of tissue sample, corresponding to the tissue sample contained in the donor block, from a sample slide is further provided. A processor is coupled to the image capture device and can receive the histol. image of the fixed section of tissue sample from the image capture device. A display is coupled to the processor for displaying the histol. image. A user interface is coupled to the control system to allow a user to select from the displayed histol. image a location for coring and removing a sample core.

L6 ANSWER 221 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:51981 CAPLUS
DN 139:21687
TI Microarray data assembler
AU Anbazhagan, Ramswamy
CS Departments of Pathology and Oncology, Johns Hopkins University School of Medicine, Baltimore, MD, 21231, USA
SO Bioinformatics (2003), 19(1), 157-158 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Large vols. of microarray data are generated and deposited in public databases. Most of this data are in the form of tab-delimited text files or Excel spreadsheets. Combing data from several of these files to reanalyze these data sets is time consuming. Microarray Data Assembler is specifically designed to simplify this task. The program can list files and data sources, convert selected text files into Excel files and assemble data across multiple Excel worksheets and workbooks. This program thus makes data assembling easy, saves time and helps avoid manual error.

L6 ANSWER 222 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:51957 CAPLUS
DN 139:21683
TI MADGE: scalable distributed data management software for cDNA microarrays
AU McIndoe, Richard A.; Lanzen, Aaron; Hurtz, Kimberly
CS Immunology and Laboratory Medicine, Department of Pathology, University of Florida, Gainesville, FL, 32610, USA
SO Bioinformatics (2003), 19(1), 87-89 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB A distributable software package, called The Microarray Database of Gene Expression (MADGE), has been designed to track and store the various pieces of data generated by a cDNA microarray facility. This includes the clone collection storage data, annotation data, work-flow queues, microarray data, data repositories, sample

submission information, and project/investigator information. This application was designed using a 3-tier client server model. The data access layer (1st tier) contains the relational database system tuned to support a large no. of transactions. The data services layer (2nd tier) is distributed COM server with full database transaction support. The application layer (3rd tier) is an Internet based user interface that contains both client and server side code for dynamic interactions with the user.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 223 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:24584 CAPLUS
DN 138:249246
TI Identification of essential and functionally moduled genes through the microarray assay
AU Rho, K.; Jeong, H.; Kahng, B.
CS School of Physics and Center for Theoretical Physics, Seoul National University, Seoul, 151-747, S. Korea
SO Los Alamos National Laboratory, Preprint Archive, Condensed Matter (2003) 1-21, arXiv:cond-mat/0301110, 9 Jan 2003 CODEN: LNCMFR URL: http://xxx.lanl.gov/pdf/cond-mat/0301110
PB Los Alamos National Laboratory
DT Preprint
LA English
AB Identification of essential genes is one of the ultimate goals of drug designs. Here we introduce an in silico method to select essential genes through the microarray assay. We construct a graph of genes, called the gene transcription network, based on the Pearson correlation coeff. of the microarray expression level. Links are connected between genes following the order of the pair-wise correlation coeffs. We find that there exist two meaningful fractions of links connected, pm and ps, where the no. of clusters becomes max. and the connectivity distribution follows a power law, cl resp. Interestingly, one of clusters at pm contains a high d. of essential genes having almost the same functionality. Thus the deletion of all genes belonging to that cluster can lead to lethal inviable mutant efficiently. Such an essential cluster can be identified in a self-organized way. Once we measure the connectivity of each gene at ps. Then using the property that the essential genes are likely to have more connectivity, we can identify the essential cluster by finding the one having the largest mean connectivity per gene at pm.
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 224 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:24024 CAPLUS
DN 138:249244
TI The importance of thermodynamic equilibrium for high throughput gene expression arrays
AU Bhanot, Gyan; Louzoun, Yoram; Zhu, Jianhua; DeLisi, Charles
CS Institute for Advanced Study, Princeton, NJ, 08540, USA
SO Biophysical Journal (2003), 84(1), 124-135 CODEN: BIOJAU; ISSN: 0006-3495
PB Biophysical Society
DT Journal
LA English
AB We present an anal. of phys. chem. constraints on the accuracy of DNA micro-arrays under equil. and nonequil. conditions. At the beginning of the article we describe an algorithm for choosing a probe set with high specificity for targeted genes under equil. conditions. The algorithm as well as existing methods is used to select probes from the full Saccharomyces cerevisiae genome, and these probe sets, along with a randomly selected set, are used to simulate array expts. and identify sources of error. Inasmuch as specificity and sensitivity are max. at thermodn. equil., we are particularly interested in the factors that affect the approach to equil. These are analyzed later in the article, where we develop and apply a rapidly executable method to simulate the kinetics of hybridization on a solid phase support. Although the difference between soln. phase and solid phase hybridization is of little consequence for specificity and sensitivity when equil. is achieved, the kinetics of hybridization has a pronounced effect on both. We first use the model to est. the effects of diffusion, cross-hybridization, relaxation time, and target concn. on the hybridization kinetics, and then investigate the effects of the most important kinetic parameters on specificity. We find even when using probe sets that have high specificity at equil. that substantial cross-hybridization is present under nonequil. conditions. Although those complexes that differ from perfect complementarity by more than a single base do not contribute to sources of error at equil., they slow the approach to equil. dramatically and confound interpretation of the data when they dissoc. on a time scale comparable to the time of the expt. For the best probe set, our simulation shows that steady-state behavior is obtained in a relaxation time of .apprx.12-15 h for exptl. target concns. .apprx.(10-13 - 10-14)M, but the time is greater for lower target concns. in the range (10-15-10-16)M. The result points to an asymmetry in the accuracy with which up- and down-regulated genes are identified.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 225 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:9647 CAPLUS
DN 138:249233
TI Modeling pharmacogenomics of the NCI-60 anticancer data set: utilizing kernel PLS to correlate the microarray data to therapeutic responses
AU Dasgupta, Nilanjan; Lin, Simon M.; Carin, Lawrence
CS Department of Electrical Engineering, Duke University, USA
SO Methods of Microarray Data Analysis II, Papers from CAMDA '01, Durham, NC, United States, Oct. 15-16, 2001 (2002), Meeting Date 2001, 151-167. Editor(s): Lin, Simon M.; Johnson, Kimberly F. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69DKZ5; ISBN: 1-4020-7111-6
DT Conference
LA English
AB Modeling the relationship between genomic features and therapeutic response is of central interest in pharmacogenomics [Musumarra et al., 2001]. The NCI-60 cancer data set with both gene expression and drug activity measurements provides an excellent opportunity for this modeling exercise. To correlate the gene expression profile with the drug activity pattern, we utilized a soft modeling technique called Partial Least Squares (PLS) [Tobias, 2000]. Soft modeling requires less stringent assumptions about the data than other modeling techniques [Falk et al., 1992]. A high level of collinearity in multi-dimensional gene expression profiles motivates us to undertake the PLS approach, which not only trims data redundancy but also exposes the underlying hidden functional units as latent features. It is believed that these functional gene groups play a key role in detg. the efficacy of the cancer drugs to different cell lines (types of cancer). We have shown the efficacy of PLS in identifying drug resistant and drug sensitive genes. We have also investigated techniques to exploit the non-linear dependence between individual gene expressions in order to explain variations in the drug activity pattern. This is facilitated by a kernel function that implicitly carries out the regression in a higher-dimensional space where the data is linear [Christiannini et al., 2000]. The kernel-based non-linear approach is shown to be more effective in defining the correlation between the drug response and the gene expressions. The PLS approach, as implemented here, could be used to differentiate cancer cell lines between renal cancer and melanoma, for example, or different drug groups like Alkylating agents and Tubulin-active anti-mitotic agents.
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 226 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:9645 CAPLUS
DN 138:249232
TI Using functional genomic units to corroborate user experiments with the Rosetta compendium
AU Lin, Simon M.; Liao, Xuejun; McConnell, Patrick; Vata, Korkut; Carin, Lawrence; Goldschmidt, Pascal
CS Duke Bioinformatics Shared Resource, Duke University Medical Center, USA
SO Methods of Microarray Data Analysis II, Papers from CAMDA '01, Durham, NC, United States, Oct. 15-16, 2001 (2002), Meeting Date 2001, 123-137. Editor(s): Lin, Simon M.; Johnson, Kimberly F. Publisher: Kluwer Academic Publishers, Norwell, Mass. CODEN: 69DKZ5; ISBN: 1-4020-7111-6
DT Conference
LA English
AB The Rosetta data set opens the possibility of comparing an exptl. microarray data set with a ref. profile from the compendium. However, explaining this comparison in terms of individual genes could be a daunting task because of the sheer no. of genes. Thus, we postulate a new strategy of modeling microarray data in terms of functional genomic units (FGUs). A functional genomic unit is a group of genes that carries out a certain biol. function. We explored the possibility of defining the functional genomic units from the Gene Ontol. (GO) annotation of the yeast genome. To visualize the tree structure of the GO, we have written a yeast genomic knowledge browser in Java, and integrated it with the microarray data. The pitfall of using the GO is that only a portion of the genes in the genome are functionally known or inferred. Thus, we further investigated an unsupervised learning method to identify those functional genomic units in the yeast genome. We have applied an established anal. method from digital signal processing, Independent Component Anal. (ICA), to the Rosetta data set. To further validate the utility of the Rosetta compendium, we have designed an expt. to investigate the yeast cells transfected with human Rac1, a small GTPase protein of the Rho family, and demonstrated that functional genomic units helped us to corroborate our own microarray expt. with the Rosetta data set.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 227 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:2381 CAPLUS
DN 138:249023
TI Signal processing techniques in genomic engineering
AU Zhang, Xin-Yu; Chen, Fei; Zhang, Yuan-Ting; Agner, Shannon C.; Akay, Metin; Lu, Zu-Hong; Waye, Mary Miu Yee; Tsui, Stephen Kwok-Wing
CS Joint Research Center for Biomedical Engineering, Chinese University of Hong Kong, Hong Kong, Peop. Rep. China
SO Proceedings of the IEEE (2002), 90(12), 1822-1833 CODEN: IEEPAD; ISSN: 0018-9219
PB Institute of Electrical and Electronics Engineers
DT Journal; General Review
LA English
AB A review. Now that the human genome has been sequenced, the measurement, processing, and anal. of specific genomic information in real time are gaining considerable interest because of their importance to better the understanding of the inherent genomic function, the early diagnosis of disease, and the discovery of new drugs. Traditional methods to process and analyze DNA (DNA) or RNA data, based on the statistical or Fourier theories, are not robust enough and are time-consuming, and thus not well suited for future routine and rapid medical applications, particularly for emergency cases. An overview of some recent applications of signal processing techniques for DNA structure prediction, detection; feature extn., and classification of differentially expressed genes is presented. Emphasis is placed on the application of wavelet transform in DNA sequence anal. and on cellular neural networks in microarray image anal., which can have a potentially large effect on the real-time realization of DNA anal. Finally, some interesting areas for possible future research are summarized, which include a biomodel-based signal processing technique for genomic feature extn.

and hybrid multidimensional approaches to process the dynamic genomic information in real time.
RE.CNT 63 THERE ARE 63 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 228 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:979676 CAPLUS
DN 138:282237
TI A System Architecture for Genomic Data Analysis
AU Glass, Aenne; Gierl, Lothar
CS Faculty of Medicine, Institute for Medical Informatics and Biometry, University of Rostock, Rostock, 18055, Germany
SO In Silico Biology (2002), 2(3), 207-211 CODEN: ISBIFC; ISSN: 1386-6338
PB IOS Press
DT Journal
LA English
AB Most diseases are caused by a set of gene defects, which occur in a complex assocn. The assocn. scheme of expressed genes can be modeled by genetic networks. Genetic networks efficiently facilitate understanding the dynamics of pathogenic processes by modeling mol. reality of cell conditions. In this sense a genetic network consists of first, a set of genes of specified cells, tissues or species, and second, causal relationships between these genes detg. the functional condition of the biol. system under disease. A relationship between two genes will exist if they both are directly or indirectly assocd. with disease [8]. Our goal is to characterize diseases (esp. autoimmune diseases like chronic pancreatitis CP, multiple sclerosis MS, rheumatoid arthritis RA) by genetic networks generated by a computer system. We want to introduce this practice as a bioinformatic approach for finding targets.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 229 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:978087 CAPLUS
DN 138:53906
TI Gene expression profiles for diagnosis of breast cancer patients and classification based on estrogen receptor and BRCA1 and prognosis
IN Dai, Hongyue; He, Yudong; Linsley, Peter S.; Mao, Mao; Roberts, Christopher J.; Van't Veer, Laura Johanna; Van de Vijver, Marc J.; Bernards, Rene; Hart, A. A. M.
PA Rosetta Inpharmatics, Inc., USA
SO PCT Int. Appl., 187 pp. CODEN: PIXXD2
DT Patent
LA English PATENT NO. KIND DATE APPLICATION NO. DATE ---------
PI WO 2002103320 A2 20021227 WO 2002-US18947 20020614 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR
PRAI US 2001-2001/PV29891U 20010618 US 2002-2002/PV380710 20020514
AB The present invention relates to genetic markers whose expression is correlated with breast cancer. Specifically, the invention provides sets of markers whose expression patterns can be used to differentiate clin. conditions assocd. with breast cancer, such as the presence or absence of the estrogen receptor ESR1, and BRCA1 and sporadic tumors, and to provide information on the likelihood of tumor distant metastases within five years of initial diagnosis. The invention relates to methods of using these markers to distinguish these conditions. The invention also relates to kits contg. ready-to-use ***microarrays*** and ***computer*** software for data anal. using the statistical methods disclosed herein.

L6 ANSWER 230 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:968515 CAPLUS
DN 138:232405
TI Discovery of causal relationships in a gene-regulation pathway from a mixture of experimental and observational DNA microarray data
AU Yoo, C.; Thorsson, V.; Cooper, G. F.
CS Center for Biomedical Informatics, University of Pittsburgh, Pittsburgh, PA, 15213, USA
SO Pacific Symposium on Biocomputing 2002, Kauai, HI, United States, Jan. 3-7, 2002 (2001), 498-509. Editor(s): Altman, Russ B. Publisher: World Scientific Publishing Co. Pte. Ltd., Singapore, Singapore. CODEN: 69DJST; ISBN: 981-02-4777-X
DT Conference
LA English
AB This paper reports the methods and results of a computer-based search for causal relationships in the gene-regulation pathway of galactose metab. in the yeast Saccharomyces cerevisiae. The search uses recently published data from cDNA microarray expts. A Bayesian method was applied to learn causal networks from a mixt. of observational and exptl. gene-expression data. The observational data were gene-expression levels obtained from unmanipulated "wild-type" cells. The exptl. data were produced by deleting ("knocking out") genes and observing the expression levels of other genes. Causal relations predicted from the anal. on 36 galactose gene pairs are reported and compared with the known galactose pathway. Addnl. exploratory analyses are also reported.
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 231 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:946898 CAPLUS
DN 138:2000
TI Microarray-based method for rapid identification of cells, microorganisms, or protein mixtures
IN Klempner, Mark S.; Pepper, Jane W.; Cunningham, Brian T.
PA USA
SO U.S. Pat. Appl. Publ., 20 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------
PI US 2002187464 A1 20021212 US 2001-957775 20010921
PRAI US 2000-234534P P 20000922 US 2001-261440P P 20010112
AB The invention provides compns. and methods for the detection, identification, and quantification of microorganisms, cells, or protein mixts. in a sample.

L6 ANSWER 232 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:946574 CAPLUS
DN 138:1996
TI Specific microarrays for breast cancer screening
IN Sauter, Edward; Dubois, Garrett
PA Thomas Jefferson University, USA
SO PCT Int. Appl., 59 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 3 PATENT NO. KIND DATE APPLICATION NO. DATE ---------
PI WO 2002099421 A2 20021212 WO 2002-US16038 20020520 WO 2002099421 A3 20031218 W: AU, CA, JP RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR
PRAI US 2001-292149P P 20010518 US 2001-340153P P 20011214 US 2001-340320P P 20011214
AB Microarrays specific for breast cancer are provided. Also provided are methods for detecting breast cancer in patients or screening therapeutics for the treatment or prevention of breast cancer by analyzing expression levels of specific genes in BECs or quantifying specific protein levels in breast ductal fluid.

L6 ANSWER 233 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:936202 CAPLUS
DN 138:216408
TI Functional bioinformatics of microarray data: from expression to regulation
AU Moreau, Yves; De Smet, Frank; Thijs, Gert; Marchal, Kathleen; De Moor, Bart
CS Department of Electrical Engineering, Katholieke Universiteit Leuven, Louvain, Belg.
SO Proceedings of the IEEE (2002), 90(11), 1722-1743 CODEN: IEEPAD; ISSN: 0018-9219
PB Institute of Electrical and Electronics Engineers
DT Journal
LA English
AB Using microarrays is a powerful technique to monitor the expression of thousands of genes in a single expt. From series of such expts., it is possible to identify the mechanisms that govern the activation of genes in an organism. Short DNA patterns (called binding sites) near the genes serve as switches that control gene expression. As a result similar patterns of expression can correspond to similar binding site patterns. Here we integrate clustering of coexpressed genes with the discovery of binding motifs. We overview several important clustering techniques and present a clustering algorithm (called adaptive quality-based clustering), which we have developed to address several shortcomings of existing methods. We overview the different techniques for motif finding, in particular the technique of Gibbs sampling, and we present several extensions of this technique in our Motif Sampler. Finally, we present an integrated web tool called INCLUSive that allows the easy anal. of microarray data for motif finding.
RE.CNT 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 234 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:909347 CAPLUS
DN 139:65635
TI Software tools for high-throughput analysis and archiving of immunohistochemistry staining data obtained with tissue microarrays
AU Liu, Chih Long; Prapong, Wijan; Natkunam, Yasodha; Alizadeh, Ash; Montgomery, Kelli; Gilks, C. Blake; van de Rijn, Matt
CS Department of Biochemistry, Stanford University Medical Center, Stanford, CA, USA
SO American Journal of Pathology (2002), 161(5), 1557-1565 CODEN: AJPAA4; ISSN: 0002-9440
PB American Society for Investigative Pathology
DT Journal
LA English
AB The creation of tissue microarrays (TMAs) allows for the rapid immunohistochem. anal. of thousands of tissue samples, with numerous different antibodies per sample. This tech. development has created a need for tools to aid in the anal. and archival storage of the large amts. of data generated. We have developed a comprehensive system for high-throughput anal. and storage of TMA immunostaining data, using a combination of com. available systems and novel software applications developed in our lab. specifically for this purpose. Staining results are recorded directly into an Excel worksheet and are reformatted by a novel program (TMA-Deconvoluter) into a format suitable for hierarchical clustering anal. or other statistical anal. Hierarchical clustering anal. is a powerful means of assessing relatedness within groups of tumors, based on their immunostaining with a panel of antibodies. Other analyses, such as generation of

survival curves, construction of Cox regression models, or assessment of intra- or interobserver variation, can also be done readily on the reformatted data. Finally, the immunoprofile of a specific case can be rapidly retrieved from the archives and reviewed through the use of Stainfinder, a novel web-based program that creates a direct link between the clustered data and a digital image database. An online demonstration of this system is available at http://genome-www.stanford.edu/TMA/explore.shtml.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 235 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:907066 CAPLUS
DN 138:1047
TI Method and system for the analysis of variance of microarray data
IN Kerr, M. Kathleen; Churchill, Gary A.
PA USA
SO U.S. Pat. Appl. Publ., 10 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2002177132 A1 20021128 US 2001-865627 20010525
PRAI US 2001-865627 20010525
AB A method for estg. the factor and interaction effects for gene expression microarray expts. is disclosed. The method requires the inversion of two square matrixes of size p and p', resp., instead of a matrix of size q where q>>p.apprxeq.p'. The factors causing variance in microarray dataset include gene-related factors, like orthogonality and other factors in the expt., and non-gene factors, like variety factor, dye factor and array factor. In particular, disclosed is a method for estg. at least one gene-variety interaction in a gene expression microarray expt. having an exptl. design characterized by a no. of degrees of freedom, q, and defined by a gene factor, a plurality of non-gene factors, a plurality of two-factor interactions wherein a full replication of genes is present for every combination of the plurality of non-gene factors, the method comprising the steps of : (a) inverting a first square matrix characterized by a size, p, wherein p<q; (b) estg. at least one of a plurality of non-gene factor effect from the first square matrix inverse; (c) constructing a second square matrix based in part on the estd. non-gene factor, the second square matrix characterized by size, p', wherein p'<q; (d) inverting a second square matrix; and (e) estg. at least one gene-variety interaction from the inverted second square matrix. Also disclosed is a method for estg. at least one gene-variety interaction in a gene expression microarray expt. generating a dataset and having a design characterized by a arrays, v varieties, n genes, and d dyes wherein a full replication of genes is present for every combination of arrays, varieties and dyes, the method comprising the steps of : (a) constructing a global data vector, d, based on a plurality of avs. of the dataset; (b) constructing a square matrix, T, characterized by a size, p, wherein p=a+v+d-3; (c) inverting the square matrix, T; (d) estg. the global effects, T, wherein T=T d; (e) constructing a square matrix, Tg, characterized by a size, p', wherein p'=p-1; (f) constructing a gene-specific data vector, dg, based on a plurality of avs. of the dataset; (g) inverting the square matrix, Tg; and (g) estg. the gene-variety interaction, .tau.g, wherein .tau.g=Tgdg. Furthermore, disclosed is a method of non-gene factor interaction wherein the transformed dataset is created according to the equation : Xijkg = Yijkgs - .mu.~ - Ai~ - Dj~ - (AD)ij, where Xijkgs is the transformed measurement of Yijkg measurement, Yijkg is the ijkgsth measurement; .upsilon.~ is the estd. mean of all measurements; Ai~ is the estd. array effect for the ith array; Dj~ is the estd. dye effect for the jth dye; (AD)ij is the estd. array-dye interaction effect of the ith array and the jth dye. The invention also includes implementation of the methods in computer software, computer readable media comprising these software instructions, and computer systems for performing the methods.

L6 ANSWER 236 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:898909 CAPLUS
DN 138:270966
TI Microarray databases: standards and ontologies
AU Stoeckert, Christian J.; Causton, Helen C.; Ball, Catherine A.
CS Center for Bioinformatics and Department of Genetics, University of Pennsylvania, Philadelphia, PA, 19104-6021, USA
SO Nature Genetics (2002), 32(Suppl.), 469-473 CODEN: NGENEC; ISSN: 1061-4036
PB Nature Publishing Group
DT Journal
LA English
AB A single microarray can provide information on the expression of tens of thousands of genes. The amt. of information generated by a microarray based expt. is sufficiently large that no single study can be expected to mine each nugget of scientific information. As a consequence, the scale and complexity of ***microarray*** expts. require that ***computer*** software programs do much of the data processing, storage, visualization, anal. and transfer. The adoption of common stds. and ontologies for the management and sharing of microarray data is essential and will provide immediate benefit to the research community.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 237 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:885679 CAPLUS
DN 138:199408
TI Part 6: cluster analysis and display
AU Spellman, Paul T.
CS University of California, Berkeley, CA, 94720-3200, USA
SO DNA Microarrays (2003), 569-581, 597-601. Editor(s): Bowtell, David; Sambrook, Joseph. Publisher: Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N. Y. CODEN: 69DHC7; ISBN: 0-87969-625-7
DT Conference
LA English
AB The goal of clustering is to organize microarray data so that the underlying structures can be recognized and explored. Four aspects of clustering gene expression are presented here (1) microarray data structure, (2) the Cluster and Tree View software packages, (3) types of clustering and math. principles, and (4) adjusting and filtering data.

L6 ANSWER 238 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:885678 CAPLUS
DN 138:353377
TI Part 5: LIMS, databases, and data management
AU Ball, Catherine A.; Sherlock, Gavin
CS Stanford Microarray Database, Stanford University School of Medicine, CA, 94305-5120, USA
SO DNA Microarrays (2003), 552-568, 597-601. Editor(s): Bowtell, David; Sambrook, Joseph. Publisher: Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N. Y. CODEN: 69DHC7; ISBN: 0-87969-625-7
DT Conference; General Review
LA English
AB A review addresses data management of the results generated from glass slide microarrays that have been spotted with DNA mols. Topics discussed include the information to be captured by a lab. information management system; requirements of results databases; and selecting database software.

L6 ANSWER 239 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:862794 CAPLUS
DN 138:181979
TI Mining microarray expression data by literature profiling
AU Chaussabel, Damien; Sher, Alan
CS Immunobiology Section, Lab. of Parasitic Diseases, National Inst. of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD, 20892, USA
SO GenomeBiology [online computer file] (2002), 3(10), No pp. given CODEN: GNBLFW; ISSN: 1465-6914 URL: http://www.genomebiology.com/content/pdf/gb-2002-3-10- research0055.pdf
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Background: The rapidly expanding fields of genomics and proteomics have prompted the development of computational methods for managing, analyzing and visualizing expression data derived from microarray screening. Nevertheless, the lack of efficient techniques for assessing the biol. implications of gene-expression data remains an important obstacle in exploiting this information. Results: To address this need, the authors have developed a mining technique based on the anal. of literature profiles generated by extg. the frequencies of certain terms from thousands of abstrs. stored in the Medline literature database. Terms are then filtered on the basis of both repetitive occurrence and co-occurrence among multiple gene entries. Finally, clustering anal. is performed on the retained frequency values, shaping a coherent picture of the functional relationship among large and heterogeneous lists of genes. Such data treatment also provides information on the nature and pertinence of the assocns. that were formed. Conclusions: The anal. of patterns of term occurrence in abstrs. constitutes a means of exploring the biol. significance of large and heterogeneous lists of genes. This approach should contribute to optimizing the exploitation of microarray technologies by providing investigators with an interface between complex expression data and large literature resources.
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 240 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:859137 CAPLUS
DN 138:131752
TI Quantitative noise analysis for gene expression microarray experiments
AU Tu, Y.; Stolovitzky, G.; Klein, U.
CS IBM T. J. Watson Research Center, Yorktown Heights, NY, 10598, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2002), 99(22), 14031-14036 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB A major challenge in DNA microarray anal. is to effectively dissoc. actual gene expression values from exptl. noise. We report here a detailed noise anal. for oligonucleotide-based microarray expts. involving reverse transcription, generation of labeled cRNA (target) through in vitro transcription, and hybridization of the target to the probe immobilized on the substrate. By designing sets of replicate expts. that bifurcate at different steps of the assay, we are able to sep. the noise caused by sample prepn. and the hybridization processes. We quant. characterize the strength of these different sources of noise and their resp. dependence on the gene expression level. We find that the sample prepn. noise is small, implying that the amplification process during the sample prepn. is relatively accurate. The hybridization noise is found to have very strong dependence on the expression level, with different characteristics for the low and high expression values. The hybridization noise characteristics at the high expression regime are mostly Poisson-like, whereas its characteristics for the small expression levels are more complex, probably due to cross-hybridization. A method to evaluate the significance of gene expression fold changes based on noise characteristics is proposed.

RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 241 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:857275 CAPLUS
DN 138:199349
TI Comparison of microarray designs for class comparison and class discovery
AU Dobbin, K.; Simon, R.
CS National Cancer Institute, Bethesda, MD, 20892, USA
SO Bioinformatics (2002), 18(11), 1438-1445 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Two-color microarray expts. in which an aliquot derived from a common RNA sample is placed on each array are called ref. designs. Traditionally, microarray expts. have used ref. designs, but designs without a ref. have recently been proposed as alternatives. We develop a statistical model that distinguishes the different levels of variation typically present in cancer data, including biol. variation among RNA samples, exptl. error and variation attributable to phenotype. Within the context of this model, we examine the ref. design and two designs which do not use a ref., the balanced block design and the loop design, focusing particularly on efficiency of ests. and the performance of cluster anal. We calc. the relative efficiency of designs when there are a fixed no. of arrays available, and when there are a fixed no. of samples available. Monte Carlo simulation is used to compare the designs when the objective is class discovery based on cluster anal. of the samples. The no. of discrepancies between the estd. clusters and the true clusters were significantly smaller for the ref. design than for the loop design. The efficiency of the ref. design relative to the loop and block designs depends on the relation between inter- and intra-sample variance. These results suggest that if cluster anal. is a major goal of the expt., then a ref. design is preferable. If identification of differentially expressed genes is the main concern, then design selection may involve a consideration of several factors.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 242 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:857271 CAPLUS
DN 138:199876
TI ARROGANT: an application to manipulate large gene collections
AU Kulkarni, Amit V.; Williams, Noelle Sevilir; Lian, Yun; Wren, Jonathan D.; Mittelman, David; Pertsemlidis, Alexander; Garner, Harold R.
CS Program in Biomedical Engineering, Southwestern Graduate School of Biomedical Science, The University of Texas Southwestern Medical Center, Dallas, TX, 75390, USA
SO Bioinformatics (2002), 18(11), 1410-1417 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB ARROGANT (ARRay OrGANizing Tool) is a software tool developed to facilitate the identification, annotation and comparison of large collections of genes or clones. The objective is to enable users to compile gene/clone collections from different databases, allowing them to design expts. and analyze the collections as well as assocd. exptl. data efficiently. ARROGANT can relate different sequence identifiers to their common ref. sequence using the UniGene database, allowing for the comparison of data from two different microarray expts. ARROGANT has been successfully used to analyze microarray expression data for colon cancer, to compile genes potentially related to cardiac diseases for subsequent resequencing (to identify single nucleotide polymorphisms, SNPs), to design a new comprehensive human cDNA microarray for cancer, to combine and compare expression data generated by different microarrays and to provide annotation for genes on custom and Affymetrix chips.
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 243 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:845238 CAPLUS
DN 138:131749
TI Observation of intermittency in gene expression on cDNA microarrays
AU Peterson, Leif E.; Lau, Kwong
CS Departments of Medicine, Molecular and Human Genetics, Baylor College of Medicine, Houston, TX, 77030, USA
SO Chemistry Preprint Server, Biochemistry (2002) 1-5, CPS: biochem/0205002, 15 May 2002 CODEN: CPSBBJ URL: http://preprint.chemweb.com/biochem/0205002
PB ChemWeb, Inc.
DT Preprint
LA English
AB The authors used scaled factorial moments to search for intermittency in the log expression ratios (LERs) for thousands of genes spotted on cDNA microarrays (gene chips). Results indicate varying levels of intermittency in gene expression. The observation of intermittency in the data analyzed provides a complimentary handle on moderately expressed genes, generally not tackled by conventional techniques.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 244 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:835116 CAPLUS
DN 138:164092
TI In silico approaches to microarray-based disease classification and gene function discovery
AU Azuaje, Francisco
CS Department of Computer Science, University of Dublin - Trinity College, Dublin, Ire.
SO Annals of Medicine (Stockholm, Sweden) (2002), 34(4), 299-305 CODEN: ANMDEU; ISSN: 0785-3890
PB Taylor & Francis
DT Journal; General Review
LA English
AB A review and discussion. The automated anal. of transcriptional profiling data promises a wealth of information that may be used to develop a more complete understanding of gene function and interactions. Moreover, it may improve the effectiveness of complex diagnostic tasks. This article discusses important data mining and management techniques to analyze genome-wide expression data. It reviews some of the major discovery goals, methods and applications in a no. of biomedical domains. Finally, this paper highlights key problems that need to be approached by a new generation of computational solns.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 245 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:824112 CAPLUS
DN 138:164210
TI A computational framework for optimal masking in the synthesis of oligonucleotide microarrays
AU Kasif, Simon; Weng, Zhiping; Derti, Adnan; Beigel, Richard; DeLisi, Charles
CS Bioinformatics Program and Biomedical Engineering Department, Center for Advanced Genomic Technology (CAGT), Boston University, Boston, MA, USA
SO Nucleic Acids Research (2002), 30(20), e106/1-e106/6 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB High-throughput genomic technologies are revolutionizing modern biol. In particular, DNA microarrays have become one of the most powerful tools for profiling global mRNA expression in different tissues and environmental conditions, and for detecting single nucleotide polymorphisms. The broad applicability of gene expression profiling to the biol. and medical realms has generated expanding demand for mass prodn. of microarrays, which in turn has created considerable interest in improving the cost effectiveness of microarray fabrication techniques. The authors have developed the computational framework for an optimal synthesis strategy for oligonucleotide microarrays. The problem was introduced by Hubbell et al. Here, the authors formalize the problem, obtain precise bounds on its complexity and devise several computational solns.
RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 246 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:823381 CAPLUS
DN 138:148295
TI Computational method for reducing variance with Affymetrix microarrays
AU Welle, Stephen; Brooks, Andrew I.; Thornton, Charles A.
CS Departments of Medicine, Pharmacology & Physiology, University of Rochester, Rochester, NY, 14642, USA
SO BMC Bioinformatics [online computer file] (2002), 3, No pp. given CODEN: BBMIC4; ISSN: 1471-2105 URL: http://www.biomedcentral.com/1471-2105/3/23
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Affymetrix microarrays are used by many labs. to generate gene expression profiles. Generally, only large differences (> 1.7-fold) between conditions have been reported. Computational methods to reduce inter-array variability might be of value when attempting to detect smaller differences. We examd. whether inter-array variability could be reduced by using data based on the Affymetrix algorithm for pairwise comparisons between arrays (ratio method) rather than data based on the algorithm for anal. of individual arrays (signal method). Six HG-U95A arrays that probed mRNA from young (21-31 yr old) human muscle were compared with six arrays that probed mRNA from older (62-77 yr old) muscle. Differences in mean expression levels of young and old subjects were small, rarely > 1.5-fold. The mean within-group coeff. of variation for 4629 mRNAs expressed in muscle was 20% according to the ratio method and 25% according to the signal method. The ratio method yielded more differences according to t-tests (124 vs. 98 differences at $P < 0.01$), rank sum tests (107 vs. 85 differences at $P < 0.01$), and the Significance Anal. of Microarrays method (124 vs. 56 differences with false detection rate < 20%; 20 vs. 0 differences with false detection rate < 5%). The ratio method also improved consistency between results of the initial scan and results of the antibody-enhanced scan. The ratio method reduces inter-array variance and thereby enhances statistical power.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 247 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:800616 CAPLUS
DN 138:132001
TI Microarray analysis of chitin elicitation in Arabidopsis thaliana
AU Ramonell, Katrina M.; Zhang, Bing; Ewing, Rob M.; Chen, Yu; Xu, Dong; Stacey, Gary; Somerville, Shauna
CS Department of Plant Biology, Carnegie Institution of Washington, Stanford, CA, 94305, USA
SO Molecular Plant Pathology (2002), 3(5), 301-311 CODEN: MPPAFD; ISSN: 1464-6722
PB Blackwell Science Ltd.
DT Journal
LA English

AB Chitin oligomers, released from fungal cell walls by endochitinase, induce defense and related cellular responses in many plants. However, little is known about chitin responses in the model plant Arabidopsis. The authors describe here a large-scale characterization of gene expression patterns in Arabidopsis in response to chitin treatment using an Arabidopsis microarray consisting of 2375 EST clones representing putative defense-related and regulatory genes. Transcript levels for 71 ESTs, representing 61 genes, were altered three-fold or more in chitin-treated seedlings relative to control seedlings. A no. of transcripts exhibited altered accumulation as early as 10 min after exposure to chitin, representing some of the earliest changes in gene expression obsd. in chitin-treated plants. Included among the 61 genes were those that have been reported to be elicited by various pathogen-related stimuli in other plants. Addnl. genes, including genes of unknown function, were also identified, broadening our understanding of chitin-elicited responses. Among transcripts with enhanced accumulation, one cluster was enriched in genes with both the W-box promoter element and a novel regulatory element. In addn., a no. of transcripts had decreased abundance, encoding several proteins involved in cell wall strengthening and wall deposition. The chalcone synthase promoter element was identified in the upstream regions of these genes, suggesting that pathogen signals may suppress the expression of some genes. These data indicate that Arabidopsis should be an excellent model to elucidate the mechanisms of chitin elicitation in plant defense.
RE.CNT 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 248 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:789399 CAPLUS
DN 138:118041
TI Exploring genetic regulatory networks in metazoan development: methods and models
AU Halfon, Marc S.; Michelson, Alan M.
CS Division of Genetics, Department of Medicine, Howard Hughes Medical Institute, Brigham and Women's Hospital, Boston, MA, 02115, USA
SO Physiological Genomics [online computer file] (2002), 10(3), 131-143 CODEN: PHGEFP; ISSN: 1094-8341 URL: http://physiolgenomics.physiology.org/cgi/reprint/10/3/131.pdf
PB American Physiological Society
DT Journal; General Review; (online computer file)
LA English
AB A review. One of the foremost challenges of 21st century biol. research will be to decipher the complex genetic regulatory networks responsible for embryonic development. The recent explosion of whole genome sequence data and of genome-wide transcriptional profiling methods, such as microarrays, coupled with the development of sophisticated computational tools for exploiting and analyzing genomic data, provide a significant starting point for regulatory network anal. In this article we review some of the main methodol. issues surrounding genome annotation, transcriptional profiling, and computational prediction of cis-regulatory elements and discuss how the power of model genetic organisms can be used to exptl. verify and extend the results of genomic research.
RE.CNT 113 THERE ARE 113 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 249 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:749178 CAPLUS
DN 138:20101
TI Bayesian hierarchical model for identifying changes in gene expression from microarray experiments
AU Broet, Philippe; Richardson, Sylvia; Radvanyi, Francois
CS Faculte de Medecine, Universite Paris XI and INSERM U472, Hopital Paul Brousse, Villejuif, 94807, Fr.
SO Journal of Computational Biology (2002), 9(4), 671-683 CODEN: JCOBEM; ISSN: 1066-5277
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB Recent developments in microarrays technol. enable researchers to study simultaneously the expression of thousands of genes from one cell line or tissue sample. This new technol. is often used to assess changes in mRNA expression upon a specified transfection for a cell line in order to identify target genes. For such expts., the range of differential expression is moderate, and teasing out the modified genes is challenging and calls for detailed modeling. The aim of this paper is to propose a methodol. framework for studies that investigate differential gene expression through microarrays technol. that is based on a fully Bayesian mixt. approach. A case study that investigated those genes that were differentially expressed in two cell lines (normal and modified by a gene transfection) is provided to illustrate the performance and usefulness of this approach.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 250 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:730667 CAPLUS
DN 137:213219
TI Network infrastructure for custom microarray synthesis and analysis
IN Anderson, Brooke P.
PA Combimatrix Corporation, USA
SO U.S., 12 pp. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 6456942 B1 20020924 US 2000-490565 20000125
PRAI US 1998-116954P P 19980125
AB The present invention provides methods for interfacing computer technol. with biol. and chem. processing and synthesis equipment. In preferred embodiments, the present invention features methods for the computer to interface with equipment useful for biol. and chem. processing and synthesis in a remote manner.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 251 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:722350 CAPLUS
DN 138:21718
TI Control analysis of DNA microarray expression data
AU Curtis, R. Keira; Brand, Martin D.
CS MRC Dunn Human Nutrition Unit, Cambridge, CB2 2XY, UK
SO Molecular Biology Reports (2002), 29(1-2), 67-71 CODEN: MLBRBU; ISSN: 0301-4851
PB Kluwer Academic Publishers
DT Journal
LA English
AB DNA microarrays produce large amts. of data. Complex changes in gene expression are revealed; sometimes thousands of mRNAs change between expts. Here we apply modular regulation anal. to microarray data to reveal and quantify the mRNA changes that are important for cellular responses. The mRNAs are sorted into clusters. How strongly a perturbation alters each cluster is multiplied by how strongly each cluster affects an output, to obtain coeffs. that describe how much of the change in the output is transmitted through each mRNA cluster. An example published dataset is analyzed to reveal that the response (relative fitness') of yeast to 2-deoxy-D-glucose is not transmitted by a single mRNA cluster, but instead many clusters contribute to the overall response. The method is applicable to microarray, transcriptome, proteome and metabolome data.
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 252 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:718459 CAPLUS
DN 138:84044
TI A maximum entropy algorithm for rhythmic analysis of genome-wide expression patterns
AU Langmead, Christopher James; McClung, C. Robertson; Donald, Bruce Randall
CS Dartmouth Computer Science Department, Hanover, NH, 03755, USA
SO Proceedings - IEEE Computer Society Bioinformatics Conference, Stanford, CA, United States, Aug. 14-16, 2002 (2002), 237-245 Publisher: IEEE Computer Society, Los Alamitos, Calif. CODEN: 69DCFT; ISBN: 0-7695-1653-X
DT Conference
LA English
AB We introduce a max. entropy-based anal. technique for extg. and characterizing rhythmic expression profiles from DNA microarray hybridization data. These patterns are clues to discovering genes implicated in cell-cycle, circadian, and other periodic biol. processes. The algorithm, implemented in a program called ENRAGE (Entropy-based Rhythmic Anal. of Gene Expression), treats the task of estg. an expression profile's periodicity and phase as a simultaneous bicriterion optimization problem. Specifically, a frequency domain spectrum is reconstructed from a time-series of gene expression data, subject to two constraints: (a) the likelihood of the spectrum and (b) the Shannon entropy of the reconstructed spectrum. Unlike Fourier-based spectral anal., max. entropy spectral reconstruction is well suited to signals of the type generated in DNA microarray expts. Our algorithm is optimal, running in linear time in the no. of expression profiles. Moreover, an implementation of our algorithm runs an order of magnitude faster than previous methods. Finally, we demonstrate that ENRAGE is superior to other methods at identifying and characterizing periodic expression profiles on both synthetic and actual DNA microarray hybridization data.
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 253 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:716531 CAPLUS
DN 137:227618
TI Device and method for detecting interactions between array oligonucleotides and target mRNA (cDNA), including use of reverse transcription, microarray technology and fluorescence resonance energy transfer
IN Estibeiro, Peter
PA Expresson Biosystems Limited, UK
SO PCT Int. Appl., 20 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2002072885 A1 20020919 WO 2002-GB1016 20020307 W: AE, AG, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, CZ, DE, DE, DK, DK, DM, DZ, EC, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG EP 1370688 A1 20031217 EP 2002-704918 20020307 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRAI GB 2001-5789 A 20010308 WO 2002-GB1016 W 20020307

AB The invention provides a device and method for detecting interactions between oligonucleotides immobilized on a solid array and mRNAs (cDNAs) that are added to the array. The invention relates that the method involves chromophore-labeled mRNAs (cDNAs) binding to array oligonucleotides labeled with a second chromophore. The invention also relates that the detection of the interaction relies on fluorescence resonance energy transfer (FRET) between the two chromophores. The invention further relates that FRET can be detected by shining an appropriate laser or other suitable controlled light source onto arrays to excite one of the matched pair of chromophores. The invention proposed that said device and method can be used for detg. structural parameters of native RNA transcripts and for detg. regions that may be effective targets for antisense mediated gene knockout.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 254 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:716517 CAPLUS
DN 137:247211
TI Methods and tools for nucleic acid sequence analysis selection and generation
IN Benight, Albert S.; Hopfinger, Anton J.; Pancoska, Petr; Riccelli, Peter V.
PA Bioinformatics DNA Codes, LLC, USA
SO PCT Int. Appl., 103 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------
------ ---- -------- ---------- --------
PI WO 2002072868 A2 20020919 WO 2002-US7439 20020311 WO 2002072868 A3 20031016 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG US 2003077607 A1 20030424 US 2002-95923 20020311
PRAI US 2001-274598P P 20010310
AB The present invention provides methods and means for analyzing, designing, selecting and generating oligomer sequences, such as those for use in multiplex array-based nucleic acid probe systems, down to the selection of a single pair of optimal primer/target oligomers. Sequences are represented by a function of sequence context, called the context functional descriptor. In addn. to the consideration of base pairing and nearest-neighbor anal., the present computational methods incorporate the use of context functional descriptors and correlation matrixes to account for higher-order thermodn. interactions between nucleic acid sequences. The Sequence Design Turbo Generator, SEQ-TG, technol. is explained and applied. The SEQ-TG is an anal. process comprised of computer-driven algorithms that utilize specified sequence-dependent input parameters and user-defined sequence constraints. It provides for de novo design of sets of nucleic acid oligomer sequences with precisely defined properties, and selection of subsets of sequences from larger sequences sets that have the desired predicted properties. SEQ-TG can be applied to generate sequences with optimum multiplex compatibility for use on microarrays or in multiplex soln. applications, or for purposes of designing optimal and unique probes and primers.

L6 ANSWER 255 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:702403 CAPLUS
DN 138:350547
TI Biotechnology around single molecule manipulation
AU Ikai, Atsushi
CS Department of Science, University of Tokyo, Midori-ku, Yokohama-shi, 226-8501, Japan
SO Nippon Kikai Gakkaishi (2002), 105(1004), 460-465 CODEN: NKGKA3; ISSN: 0021-4728
PB Nippon Kikai Gakkai
DT Journal; General Review
LA Japanese
AB A review. Biotechnol. break-through to promote research on single biomol. was discussed. The coverage of the topics included DNA chip/ ***microarray*** technologies, protein engineering, lob on a chip technol., use of ***computer*** simulation and bioinformatics.

L6 ANSWER 256 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:696997 CAPLUS
DN 137:365699
TI Can replication save noisy microarray data?
AU Wernisch, Lorenz
CS School of Crystallography, Birkbeck College, London, WC1E 7HX, UK
SO Comparative and Functional Genomics (2002), 3(4), 372-374 CODEN: CFGOAT; ISSN: 1531-6912
PB John Wiley & Sons Ltd.
DT Journal; General Review
LA English
AB A review. Microarray expts. are multi-step processes. At each step - the growth of cultures, extn. of mRNA, reverse transcription, labeling, hybridization, scanning, and image anal. - variation and error cannot be completely avoided. Estg. the amt. of such noise and variation is essential, not only to test for differential expression but also to suggest at which level replication is most effective. Replication and averaging are the key to the estn. as well as the redn. of variability. Here I discuss the use of ANOVA mixed models and of anal. of variance components as a rigorous way to calc. the no. of replicates necessary to detect a given target fold-change in expression levels.
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 257 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:696996 CAPLUS
DN 137:365698
TI B.mu.G@Sbase - a microarray database and analysis tool
AU Witney, Adam A.; Hinds, Jason
CS Bacterial Microarray Group, Department of Medical Microbiology, St George's Hospital Medical School, London, SW17 0RE, UK
SO Comparative and Functional Genomics (2002), 3(4), 369-371 CODEN: CFGOAT; ISSN: 1531-6912
PB John Wiley & Sons Ltd.
DT Journal; General Review
LA English
AB A review. The manuf. and use of a whole-genome microarray is a complex process and it is essential that all data surrounding the process is stored, is accessible and can be easily assocd. with the data generated following hybridization and scanning. As part of a program funded by the Wellcome Trust, the Bacterial Microarray Group at St. George's Hospital Medical School (B.mu.G@S) will generate whole-genome microarrays for 12 bacterial pathogens for use in collaboration with specialist research groups. B.mu.G@S will collaborate with these groups at all levels, including the exptl. design, methodol. and anal. In addn., we will provide informatic support in the form of a database system (B.mu.G@Sbase). B.mu.G@Sbase will provide access through a web interface to the microarray design data and will allow individual users to store their data in a searchable, secure manner. Tools developed by B.mu.G@S in collaboration with specific research groups investigating anal. methodol. will also be made available to those groups using the arrays and submitting data to B.mu.G@Sbase.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 258 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:684929 CAPLUS
DN 138:21711
TI Determination of minimum sample size and discriminatory expression patterns in microarray data
AU Hwang, Daehee; Schmitt, William A.; Stephanopoulos, George; Stephanopoulos, Gregory
CS Department of Chemical Engineering, Massachusetts Institute of Technology, Cambridge, MA, 02139, USA
SO Bioinformatics (2002), 18(9), 1184-1193 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Motivation: Transcriptional profiling using microarrays can reveal important information about cellular and tissue expression phenotypes, but these measurements are costly and time consuming. Addnl., tissue sample availability poses further constraints on the no. of arrays that can be analyzed in connection with a particular disease or state of interest. It is therefore important to provide a method for the detn. of the min. no. of microarrays required to sep., with statistical reliability, distinct disease states or other physiol. differences. Results: Power anal. was applied to est. the min. sample size required for two-class and multi-class discrimination. The power anal. algorithm calcs. the appropriate sample size for discrimination of phenotypic subtypes in a reduced dimensional space obtained by Fischer discriminant anal. (FDA). This approach was tested by applying the algorithm to existing data sets for estn. of the min. sample size required for drawing certain conclusions on multi-class distinction with statistical reliability. It was confirmed that when the min. no. of samples estd. from power anal. is used, group means in the FDA discrimination space are statistically different.
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 259 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:682603 CAPLUS
DN 138:20096
TI Evaluating test statistics to select interesting genes in microarray experiments
AU Kooperberg, Charles; Sipione, Simonetta; LeBlanc, Michael; Strand, Andrew D.; Cattaneo, Elena; Olson, James M.
CS Division of Public Health Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA, 98109-1024, USA
SO Human Molecular Genetics (2002), 11(19), 2223-2232 CODEN: HMGEE5; ISSN: 0964-6906
PB Oxford University Press
DT Journal
LA English
AB A randomization procedure to evaluate the significance level and the false-discovery rate in complex microarray expts. is proposed. A related graph can be used to compare different test statistics that can be used to analyze the same expt. This graph is closely related to receiver operator characteristic (ROC) curves. The proposed method is applied to a subset of the data from a cell-line expt. related to Huntington's disease. A small simulation study compares the effectiveness of the proposed procedure with the significance anal. of microarrays (SAM) procedure.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 260 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:666399 CAPLUS
DN 137:348693
TI MArray: analyzing single, replicated or reversed microarray experiments

AU Wang, Junbai; Nygaard, Vigdis; Smith-Sorensen, Birgitte; Hovig, Eivind; Myklebost, Ola
CS Department of Tumour Biology, Norwegian Radium Hospital, Oslo, N0310, Norway
SO Bioinformatics (2002), 18(8), 1139-1140 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Summary: MArray is a Matlab toolbox with a graphical user interface that allows the user to analyze single or paired microarray datasets by direct input of the raw data output file from image anal. packages, such as QuantArray or GenePiX. The application provides simple procedures to manually evaluate the quality of each measurement, multiple approaches to both ratio normalization (simple normalization, intensity dependent normalization) and evaluation of the reproducibility of paired expts. (using the techniques simple statistical method' and quality control ellipse' and significance anal. of microarrays'). Specifically, interactive spot evaluation functions are available in MArray and an online gene information database (NCBI UniGene) is linked. The application may provide a valuable aid in selecting and optimizing exptl. procedures, as well as serving as an anal. tool for two-state biol. comparisons, such as a study of single-dose activation. It is entirely platform independent, and only requires Matlab installed.
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 261 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:637796 CAPLUS
DN 137:164655
TI Identification and characterization of genes using microarrays
IN Linsley, Peter S.; Biery, Matthew; Mao, Mao
PA Rosetta Inpharmatics, Inc., USA
SO PCT Int. Appl., 73 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2002064743 A2 20020822 WO 2002-US4219 20020212 WO 2002064743 A3 20021031 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG AU 2002250066 A1 20020828 AU 2002-250066 20020212
PRAI US 2001-268173P P 20010212 WO 2002-US4219 W 20020212
AB The invention relates to methods and systems (e.g., computer systems and ***computer*** program products) for identifying and characterizing genes using ***microarrays*** . In particular, the invention provides for improved, robust methods for detecting genes through the use of microarrays to analyze the expression state of the genome. Genes which are expressed can be mapped to their resp. positions in the genome, and the structure of such genes can be detd. Thus, microarrays enable an efficient and comprehensive genome scan that provides much more detailed data than prior art methods. The method allows for the efficient identification of small genes, genes that do not encoded proteins, genes that are transcribed at low levels, and untranslated regions of mRNAs encoding proteins. The use of microarrays allows the structure of the gene to be detd. at the same time as the gene is detected, even if the gene is spread over larger regions of the genome. Addnl., the method allows for the verification of the exon content of a transcript of a particular gene through the use of PCR. The method was applied first to known regions of the human CXCR4 and Rb genes, then to chromosome 22, in order to identify all exons present. Finally, the method was used to survey the entire human genome.

L6 ANSWER 262 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:632409 CAPLUS
DN 138:67181
TI The microarray: potential applications for ophthalmic research
AU Wilson, Ann S.; Hobbs, Bridget G.; Speed, Terence P.; Rakoczy, P. Elizabeth
CS Department of Molecular Ophthalmolgy, Lions Eye Institute, University of Western Australia, Nedlands, WA, Australia
SO Molecular Vision [online computer file] (2002), 8, 259-270 CODEN: MVEPFB; ISSN: 1090-0535 URL: http://www.molvis.org/molvis/v8/a33/wilson.pdf
PB Molecular Vision
DT Journal; General Review; (online computer file)
LA English
AB A review. The ***microarray*** is a revolutionary technol. combining mol. biol. and ***computer*** technol. in the high throughput, simultaneous anal. of global gene expression. It is emerging as a powerful and valuable research tool that holds great promise in elucidating the mol. mechanisms involved in complex diseases. The information gained may provide direction toward identifying appropriate targets for therapeutic intervention. Despite the enormous potential of this technol., however, a no. of issues exist that complicate gene expression anal. and require further resoln. This paper reviews these issues as well as the conceptual, practical and statistical aspects of microarray technol., including its current use in research and clin. applications. Furthermore, the advantages and potential benefits of this technol. in ophthalmic research are discussed, with particular attention to retinal diseases, and its possible application in the identification of genes involved in ocular disease progression that may serve as clin. markers or potential therapeutic targets.
RE.CNT 67 THERE ARE 67 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 263 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:602957 CAPLUS
DN 137:320937
TI Deriving quantitative conclusions from microarray expression data
AU Olshen, Adam B.; Jain, Ajay N.
CS Comprehensive Cancer Center, Cancer Research Institute, University of California, San Francisco, CA, 94143-0128, USA
SO Bioinformatics (2002), 18(7), 961-970 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB The last few years have seen the development of DNA microarray technol. that allows simultaneous measurement of the expression levels of thousands of genes. While many methods have been developed to analyze such data, most have been visualization-based. Methods that yield quant. conclusions have been diverse and complex. The authors present two straightforward methods for identifying specific genes whose expression is linked with a phenotype or outcome variable as well as for systematically predicting sample class membership:. (1) A conservative, permutation-based approach to identifying differentially expressed genes;. (2) An augmentation of K-nearest-neighbor pattern classification. The analyses replicate the quant. conclusions of Golub et al. (Science, 286, 531-537, 1999) on leukemia data, with better classification results, using far simpler methods. With the breast tumor data of Perou et al. (Nature, 406, 747-752,2000), the methods lend rigorous quant. support to the conclusions of the original paper. In the case of the lymphoma data in Alizadeh et al. (Nature, 403, 503-511,2000), the analyses only partially support the conclusions of the original authors. The software and supplementary information are available freely to researchers at academic and nonprofit institutions at http://cc.ucsf.edu/jain/public.
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 264 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:597018 CAPLUS
DN 138:67763
TI Normalization and analysis of DNA microarray data by self-consistency and local regression
AU Kepler, Thomas B.; Crosby, Lynn; Morgan, Kevin T.
CS Santa Fe Institute, Santa Fe, NM, 87501, USA
SO GenomeBiology [online computer file] (2002), 3(7), No pp. given CODEN: GNBLFW; ISSN: 1465-6914 URL: http://genomebiology.com/2002/3/7/research/0037.1
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Background: With the advent of DNA hybridization microarrays comes the remarkable ability, in principle, to simultaneously monitor the expression levels of thousands of genes. The quant. comparison of two or more microarrays can reveal, for example, the distinct patterns of gene expression that define different cellular phenotypes or the genes induced in the cellular response to insult or changing environmental conditions. Normalization of the measured intensities is a prerequisite of such comparisons, and indeed, of any statistical anal., yet insufficient attention has been paid to its systematic study. The most straightforward normalization techniques in use rest on the implicit assumption of linear response between true expression level and output intensity. We find that these assumptions are not generally met, and that these simple methods can be improved. Results: We have a robust semi-parametric normalization technique based on the assumption that the large majority of genes will not have their relative expression levels changed from one treatment group to the next, and on the assumption that departures of the response from linearity are small and slowly varying. We use local regression to est. the normalized expression levels as well as the expression level-dependent error variance. Conclusions: We illustrate the use of this technique in a comparison of the expression profiles of cultured rat mesothelioma cells under control and under treatment with potassium bromate, validated using quant. PCR on a selected set of genes. We tested the method using data simulated under various error models and find that it performs well.
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 265 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:597014 CAPLUS
DN 138:67762
TI A prediction-based resampling method for estimating the number of clusters in a dataset
AU Dudoit, Sandrine; Fridlyand, Jane
CS Division of Biostatistics, School of Public Health, University of California Berkeley, Berkeley, CA, 94720-7360, USA
SO GenomeBiology [online computer file] (2002), 3(7), No pp. given CODEN: GNBLFW; ISSN: 1465-6914 URL: http://genomebilogy.com/2002/3/7/research.0036.1
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Background: Microarray technol. is increasingly being applied in biol. and medical research to address a wide range of problems, such as the classification of tumors. An important statistical problem assocd. with tumor classification is the identification of new tumor classes using gene-expression profiles. Two essential aspects of this clustering problem are: to est. the no. of clusters, if any, in a dataset; and to allocate tumor samples to these clusters, and assess the confident of cluster assignments for individual samples. Here we address the first of these problems. Results: We have developed a new prediction-based reampling method, Clest, to est. the no. of clusters in a dataset. The performance of the new and existing methods were compared using ***simulated*** data and gene-expression data from four recently published cancer

microarray studies. Clest was generally found to be more accurate and robust than the six existing methods considered in the study.
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 266 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:595322 CAPLUS
DN 137:121955
TI Systems and ***computer*** software products for comparing ***microarray*** spot intensities
IN Bartell, Daniel M.; Liu, Wei-min
PA USA
SO U.S. Pat. Appl. Publ., 16 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2002106117 A1 20020808 US 2000-737536 20001213
PRAI US 2000-737536 20001213
AB Methods, systems and computer software products are provided for analyzing gene expression data using pixel intensities.

L6 ANSWER 267 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:580251 CAPLUS
DN 138:101424
TI ***Simulation*** of cDNA ***microarrays*** via a parameterized random signal model
AU Balagurunathan, Yoganand; Dougherty, Edward R.; Chen, Yidong; Bittner, Michael L.; Trent, J. M.
CS Department of Electrical Engineering, Texas A&M University, College Station, TX, 77843-3128, USA
SO Journal of Biomedical Optics (2002), 7(3), 507-523 CODEN: JBOPFO; ISSN: 1083-3668
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
AB CDNA microarrays provide simultaneous expression measurements for thousands of genes that are the result of processing images to recover the av. signal intensity from a spot composed of pixels covering the area upon which the cDNA detector has been put down. The accuracy of the signal measurement depends on using an appropriate algorithm to process the images. This includes detg. spot locations and processing the data in such a way as to take into account spot geometry, background noise, and various kinds of noise that degrade the signal. This paper presents a stochastic model for microarray images. There are over 20 model parameters, each governed by a probability distribution, that control the signal intensity, spot geometry, spot drift, background effects, and the many kinds of noise that affect microarray images owing to the manner in which they are formed. The model can be used to analyze the performance of image algorithms designed to measure the true signal intensity because the ground truth (signal intensity) for each spot is known. The levels of foreground noise, background noise, and spot distortion can be set, and algorithms can be evaluated under varying conditions.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 268 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:575791 CAPLUS
DN 137:104767
TI System and computer software products for comparative gene expression analysis
IN Liu, Wei-min; Di, Xiaojun
PA USA
SO U.S. Pat. Appl. Publ., 16 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2002103604 A1 20020801 US 2000-735574 20001212
PRAI US 2000-735574 20001212
AB Methods and computer software products are provided for analyzing gene expression data. In one embodiment, methods, systems and computer software are provided for comparative gene expression anal. using intensity dependent normalization factors.

L6 ANSWER 269 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:565464 CAPLUS
DN 138:50755
TI Interpreting microarray data to build models of microbial genetic regulation networks
AU Sokhansanj, Bahrad A.; Garnham, Janine B.; Fitch, J. Patrick
CS Biology & Biotechnology Research Program, Lawrence Livermore National Laboratory, University of California, Livermore, CA, 94550, USA
SO Proceedings of SPIE-The International Society for Optical Engineering (2002), 4623(Functional Monitoring and Drug-Tissue Interaction), 27-37 CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
AB Microarrays and DNA chips are an efficient, high-throughput technol. for measuring temporal changes in the expression of message RNA (mRNA) from thousands of genes (often the entire genome of an organism) in a single expt. A crucial drawback of microarray expts. is that results are inherently qual.: data are generally neither quant. repeatable, nor may microarray spot intensities be calibrated to in vivo mRNA concns. Nevertheless, microarrays represent by the far the cheapest and fastest way to obtain information about a cell's global genetic regulatory networks. Besides poor signal characteristics, the massive no. of data produced by microarray expts. pose challenges for visualization, interpretation and model building. Towards initial model development, we have developed a Java tool for visualizing the spatial organization of gene expression in bacteria. We are also developing an approach to inferring and testing qual. fuzzy logic models of gene regulation using microarray data. Because we are developing and testing qual. hypotheses that do not require quant. precision, our statistical evaluation of exptl. data is limited to checking for validity and consistency. Our goals are to maximize the impact of inexpensive microarray technol., bearing in mind that biol. models and hypotheses are typically qual.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 270 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:564605 CAPLUS
DN 137:380553
TI An algorithm for finding protein-DNA binding sites with applications to chromatin-immunoprecipitation microarray experiments
AU Liu, X. Shirley; Brutlag, Douglas L.; Liu, Jun S.
CS Stanford Medical Informatics, Stanford University, Stanford, CA, 94305, USA
SO Nature Biotechnology (2002), 20(8), 835-839 CODEN: NABIF9; ISSN: 1087-0156
PB Nature Publishing Group
DT Journal
LA English
AB Chromatin immunopptn. followed by cDNA microarray hybridization (ChIP-array) has become a popular procedure for studying genome-wide protein-DNA interactions and transcription regulation. However, it can only map the probable protein-DNA interaction loci within 1-2 kilobases resoln. To pinpoint interaction sites down to the base-pair level, we introduce a computational method, Motif Discovery scan (MDscan), that examines the ChIP-array-selected sequences and searches for DNA sequence motifs representing the protein-DNA interaction sites. MDscan combines the advantages of two widely adopted motif search strategies, word enumeration and position-sp. wt. matrix updating, and incorporates the ChIP-array ranking information to accelerate searches and enhance their success rates. MDscan correctly identified all the exptl. verified motifs from published ChIP-array expts. in yeast (STE12, GAL4, RAP1, SCB, MCB, MCM1, SFF, and SWI5), and predicted two motif patterns for the differential binding of Rap1 protein in telomere regions. In our studies, the method was faster and more accurate than several established motif-finding algorithms. MDscan can be used to find DNA motifs not only in ChIP-array expts. but also in other expts. in which a subgroup of the sequences can be inferred to contain relatively abundant motif sites. The MDscan web server can be accessed at http://BioProspector.stanford.edu/MDs can/.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 271 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:541715 CAPLUS
DN 137:154521
TI Efficient evaluation of microarrays
AU Werenskiold, Anne Katrin
CS Axxima Pharmaceuticals AG, Martinsried, 82152, Germany
SO GIT Labor-Fachzeitschrift (2002), 46(3), 297-299 CODEN: GLFAF5
PB GIT Verlag GmbH & Co. KG
DT Journal
LA German
AB The computer program ScreenBase based on FileMaker 5.5 is described. The software was developed to evaluate high-throughput data of the microarray technique.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 272 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:520880 CAPLUS
DN 137:352402
TI Arrayplot for visualization and normalization of cDNA microarray data
AU Marc, Philippe; Jacq, Claude
CS Laboratoire de Genetique Moleculaire (UMR CNRS 8541) Ecole Normale Superieure, Paris, 75005, Fr.
SO Bioinformatics (2002), 18(6), 888-889 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Arrayplot is an application which allows filtering, visualization and normalization of raw cDNA microarray data.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 273 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:515145 CAPLUS
DN 137:181876
TI Spreading diagrams for the optimization of quill pin printed microarray density
AU Smith, Jason T.; Viglianti, Benjamin L.; Reichert, W. Monty
CS Department of Biomedical Engineering, Duke University, Durham, NC, 27708, USA
SO Langmuir (2002), 18(16), 6289-6293 CODEN: LANGD5; ISSN: 0743-7463
PB American Chemical Society
DT Journal
LA English

AB The printed feature size from a quill pin microarraying system was characterized to predict optimal microarray d. from common exptl. variables of pin size, soln. viscosity, and surface wettability. Features contg. fluorescent dye were printed from two solvent systems, glycerol in water and sucrose in water, and obsd. over a wide range of solute concns. and substrate wettabilities. Obsd. feature spreading was used to generate spreading diagrams that predict printed microarray feature dimensions from the water contact angle of the substrate, the size of the printing pin, and the viscosity (or wt % solute) of the printing buffer. In general, feature size was obsd. to increase with substrate wettability and soln. viscosity. A simple model was developed to predict feature d. as a function of the above variables.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 274 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:513699 CAPLUS
DN 138:19980
TI Forefront of development of DNA microarray apparatus
AU Kondo, Naoto
CS Life Science Business Unit, Yokogawa Analytical Systems Co., Ltd., Japan
SO Biobencha (2002), 2(3), 51-57 CODEN: BIOBC8; ISSN: 1346-5376
PB Yodosha
DT Journal; General Review
LA Japanese
AB A review. The use of high d. DNA microarray is crit. for processing a large no. of samples for DNA genome-wide anal. This review paper discussed technol. implementation necessary for supporting such high d. DNA microarray systems. Development of the accurate microarray scanner with a dynamic auto-focus system for homogeneous scanning and the laser irradn. system with automatic laser intensity controller were described. Development of a ***computer*** software for quantitating ***microarray*** signals was also described regarding the topics on spot detn. by gridding, pixel cutting and background correction.

L6 ANSWER 275 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:507597 CAPLUS
DN 137:323255
TI Application of cDNA microarrays to generate a molecular taxonomy capable of distinguishing between colon cancer and normal colon
AU Zou, Tong-Tong; Selaru, Florin M.; Xu, Yan; Shustova, Valentina; Yin, Jing; Mori, Yuriko; Shibata, David; Sato, Fumiaki; Wang, Suma; Olaru, Andreea; Deacu, Elena; Liu, Thomas C.; Abraham, John M.; Meltzer, Stephen J.
CS Department of Medicine, University of Maryland School of Medicine and Baltimore VA Hospital, Division of Gastroenterology and Greenebaum Cancer Center, Baltimore, MD, 21201, USA
SO Oncogene (2002), 21(31), 4855-4862 CODEN: ONCNES; ISSN: 0950-9232
PB Nature Publishing Group
DT Journal
LA English
AB In order to discover global gene expression patterns characterizing subgroups of colon cancer, microarrays were hybridized to labeled RNAs obtained from seventeen colonic specimens (nine carcinomas and eight normal samples). Using a hierarchical agglomerative method, the samples grouped naturally into two major clusters, in perfect concordance with pathol. reports (colon cancer vs. normal colon). Using a variant of the unpaired t-test, selected genes were ordered according to an index of importance. In order to confirm microarray data, we performed quant., real-time reverse transcriptase-polymerase chain reaction (TaqMan RT-PCR) on RNAs from 13 colorectal tumors and 13 normal tissues (seven of which were matched normal-tumor pairs). RT-PCR was performed on the gro1, B-factor, adlican, and endothelin converting enzyme-1 genes and confirmed microarray findings. Two hundred and fifty genes were identified, some of which were previously reported as being involved in colon cancer. We conclude that cDNA microarraying, combined with bioinformatics tools, can accurately classify colon specimens according to current histopathol. taxonomy. Moreover, this technol. holds promise of providing invaluable insight into specific gene roles in the development and progression of colon cancer. Our data suggests that a large-scale approach may be undertaken with the purpose of identifying biomarkers relevant to cancer progression.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 276 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:489967 CAPLUS
DN 138:148219
TI XPAK: A visualization toolkit for transcriptome analysis
AU Masuda, Yasushi; Kanaya, Shigehiko; Mori, Hirotada
CS Japan Science and Technology Corporation, Kagauchi, Saitama, 332-0012, Japan
SO Genome Informatics Series (2001), 12, 464-465 CODEN: GINSE9; ISSN: 0919-9454
PB Universal Academy Press
DT Journal
LA English
AB A web-based visualization toolkit, called XPAK (eXPression Anal. Kit), has been developed which supports several primitive visualization toolkits including interactive comparison of microarray data. XPAK enables the rapid evaluation of exptl. results and the construction of web sites for publication. It consists of a database storing fundamental descriptions of all genes on the target organism and microarray expression data, and a web-based front-end system for data anal. and visualization.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 277 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:489880 CAPLUS
DN 137:364283
TI A network-based array data interpreter
AU Nakata, Kotoko; Toda, Kyoko; Ichiishi, Eiichiro; Kaminuma, Tsuguchika
CS Division of Chem-Bio Informatics, National Institute of Health Sciences, Setagaya-ku, Tokyo, 158-8501, Japan
SO Genome Informatics Series (2001), 12, 261-262 CODEN: GINSE9; ISSN: 0919-9454
PB Universal Academy Press
DT Journal
LA English
AB A network-based array analyses data interpreter was developed using the GeneSpring com. software package and the Cell Signaling Networks Database (CSNDB). The data interpreter has been used to analyze several DNA chips.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 278 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:489865 CAPLUS
DN 137:364282
TI GeneSpring: Tools for analyzing microarray expression data
AU Chu, Lillian; Scharf, Eric; Kondo, Takashi
CS Silicon Genetics, Redwood City, CA, 94063, USA
SO Genome Informatics Series (2001), 12, 227-229 CODEN: GINSE9; ISSN: 0919-9454
PB Universal Academy Press
DT Journal
LA English
AB The set of tools that comprise GeneSpring as a means to survey current methods of anal. is presented. GeneSpring comes with an intuitive interface incorporating organized file management, handles data from multiple array formats, includes multiple data display formats, a suite of statistical clustering tools, and incorporates automated annotation and cross-referencing. The GeneSpring interface is const. among the Windows, Macintosh and UNIX platforms on which it is available.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 279 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:489845 CAPLUS
DN 138:50366
TI Minimum spanning trees for gene expression data clustering
AU Xu, Ying; Olman, Victor; Xu, Dong
CS Life Sciences Division, Oak Ridge National Laboratory, Computational Protein Structure Group, Oak Ridge, TN, 27831-6480, USA
SO Genome Informatics Series (2001), 12, 24-33 CODEN: GINSE9; ISSN: 0919-9454
PB Universal Academy Press
DT Journal
LA English
AB This paper describes a new framework for microarray gene-expression data clustering. The foundation of this framework is a min. spanning tree (MST) representation of a set of multi-dimensional gene expression data. A key property of this representation is that each cluster of the expression data corresponds to one subtree of the MST, which, rigorously converts a multi-dimensional clustering problem to a tree partitioning problem. We have demonstrated that though the inter-data relationship is greatly simplified in the MST representation, no essential information is lost for the purpose of clustering. Two key advantages in representing a set of multi-dimensional data as an MST are: (1) the simple structure of a tree facilitates efficient implementations of rigorous clustering algorithms, which otherwise are highly computationally challenging; and (2) as an MST-based clustering does not depend on detailed geometric shape of a cluster, it can overcome many of the problems faced by classical clustering algorithms. Based on the MST representation, we have developed a no. of rigorous and efficient clustering algorithms, including two with guaranteed global optimality. We have implemented these algorithms as a computer software EXCAVATOR. To demonstrate its effectiveness, we have tested it on two data sets, i.e., expression data from yeast Saccharomyces cerevisiae, and Arabidopsis expression data in response to chitin elicitation.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 280 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:489838 CAPLUS
DN 138:169511
TI Efficient evaluation of microarrays
AU Werenskiold, Anne Katrin
CS Axxima Pharmaceutical AG, Martinsried, D-82152, Germany
SO Bioforum International (2002), 6(3), 139-141 CODEN: BINTFQ; ISSN: 1434-2693
PB GIT Verlag GmbH
DT Journal
LA English
AB The increasing use of microarrays has brought about a massive increase in the large vols. of data generated in mol. biol. labs. over the past few years. The software package "Screen-Base", based on "File-Maker Pro" as the development system, is making headway through the data jungle, developed by the Hamburg company Busch-EDV under contract to the Martinsried biotechnol. company Axxima Pharmaceuticals.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 281 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:489253 CAPLUS

DN 137:243031
TI A bioinformatics tool to select sequences for microarray studies of mouse models of oncogenesis
AU Edgerton, Mary E.; Taylor, Ronald; Powell, John I.; Hunter, Lawrence; Simon, Richard; Liu, Edison T.
CS Department of Pathology and Laboratory Medicine, Hospital of the University of Pennsylvania, Philadelphia, PA, 19104, USA
SO Bioinformatics (2002), 18(5), 774-775 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB One of the challenges to the effective utilization of cDNA microarray anal. in mouse models of oncogenesis is the choice of a crit. set of probes that are informative for human disease. Given the thousands of genes with a potential role in human oncogenesis and the hundreds of thousands of mouse sequences available for use as probes, selection of an informative set of mouse probes can be an overwhelming task. We have developed a web based sequence mining tool using DataBase Independent (DBI) Perl to annotate publicly available sequences. The Mouse Oncochip Design Tool uses the Mouse Genome Database (MGD) developed and maintained by the Jackson Labs. for mouse DNA sequences. There are over 380 000 sequences in their database. The output list has been ordered to present the genes more likely to be informative in a mouse model of human cancer using a candidate set of oncogenes to order the list. Mouse sequences that represent genes that are homologous with a member of a human oncogene set are listed first. In addn. it provides a set of links for information on clone source gene function.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 282 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:466336 CAPLUS
DN 137:29017
TI Multiple regression analysis of correlations between genes from microarray gene expression data
IN Kishino, Hirohisa; Waddell, Peter
PA Japan as Represented by the President of the University of Tokyo, Japan; Chugai Seiyaku Kabushiki Kaisha
SO PCT Int. Appl., 52 pp. CODEN: PIXXD2
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2002048915 A1 20020620 WO 2001-JP10780 20011210 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG AU 2002021104 A5 20020624 AU 2002-21104 20011210
PRAI JP 2000-375381 A 20001211 WO 2001-JP10780 W 20011210
AB A method of detecting a correlation between genes involving the step wherein a partial correlation coeff. is approx. detd. with the use of regression anal. in assocn. with selection of variables to thereby eliminate effects of an arbitrary third gene on a first and second genes among a large no. of genes. Thus, the relation between the first and second genes can be found out without affected by any other gene. This method is useful in analyzing the expression profile of genes obtained by DNA microarrays. Anal. of correlations between 44 genes whose expression differs between cancer and normal cells is described.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 283 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:459679 CAPLUS
DN 137:29983
TI Spotting of microarrays with elective re-formatting of samples
AU Fiehn, Hendrik; Burger, Mario; Hoffmann, Peter; Gehring, Thomas
CS GeSiM mbH, Grosserkmannsdorf, D-01454, Germany
SO BIOspektrum (2002), 8(2), 205-206 CODEN: BOSPFD; ISSN: 0947-0867
PB Spektrum Akademischer Verlag
DT Journal
LA German
AB The arraying of samples is introduced on application-specific carriers using the contact (simultaneous pipetting) or non-contact spotting procedure. The software for the controlling of the microspotter system is described.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 284 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:448983 CAPLUS
DN 137:242639
TI ***Microarray*** Assistant clone organizer and array ***simulator***
AU Anbazhagan, Ramaswamy
CS The Johns Hopkins University School of Medicine, Baltimore, MD, USA
SO BioTechniques (2002), 32(6), 1398-1402 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
AB Microarrays are extensively used in mol. biol. expts. While several vendors offer microarrays on a variety of platforms, many researchers prefer to use custom microarrays with a selected list of clones for their expts. Many research centers have established core facilities for the prodn. of custom microarrays. Microarray prodn. involves a no. of steps, including maintaining a master list of stock clones, selecting required clones for custom microarrays, subculturing selected clones, amplifying inserts, recording results, and identifying the orientation of clones in the microarray. The authors have created a simple, user-friendly, and versatile Microsoft Excel spreadsheet-based software, Microarray Assistant, which can assist the user in all the steps of microarray design and synthesis. In addn., the program gives options to insert, delete, or interchange clones during various steps. The program also gives a visual picture of the locations of the clones in the plates, as well as in the microarray. The program can also be used to assist in the transfer of clones between plates of different configuration.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 285 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:448982 CAPLUS
DN 137:227135
TI Automatic quantitation of hybridization signals on cDNA arrays
AU Tahi, F.; Achddou, B.; Decraene, C.; Alibert, O.; Guiot, H.; Auffray, C.; Pietu, G.
CS CNRS FRE 2376, Genexpress, Villejuif, Fr.
SO BioTechniques (2002), 32(6), 1386-1388, 1390, 1392, 1394, 1396-1397 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
AB Large-scale hybridization of simple or complex cDNA probes to cDNA clones arrayed on high-d. filters is a method frequently used to det. systematically the expression profiles of thousands of genes. Hybridization signal intensities, which reflect the level of transcription of the corresponding genes, are captured on phosphor screens with an imaging system. We describe a high-throughput system, Xdots-Reader, that performs automatic detection and quantitation of each signal on hundreds of images. Reproducibility of spot detection and quantitation within filters and between filters has been assessed in anal. of more than 850 000 hybridization signals on 436 filters. The automatic anal. success was greater than 97%, with 424 of the 436 tested filters fully analyzed without any human intervention. It runs on SUN workstations under UNIX (SunOS or Solaris) and on PC under LINUX. No particular hardware is required, and the software is compatible with any other software. It supports the main std. image formats.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 286 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:448973 CAPLUS
DN 137:227130
TI Local mean normalization of microarray element signal intensities across an array surface: quality control and correction of spatially systematic artifacts
AU Colantuoni, Carlo; Henry, George; Zeger, Scott; Pevsner, Jonathan
CS Kennedy Krieger Institute, Johns Hopkins University School of Medicine, Baltimore, MD, USA
SO BioTechniques (2002), 32(6), 1316-1320 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
AB Here we present a methodol. for the normalization of element signal intensities to a mean intensity calcd. locally across the surface of a DNA microarray. These methods allow the detection and/or correction of spatially systematic artifacts in microarray data. These include artifacts that can be introduced during the robotic printing, hybridization, washing, or imaging of microarrays. Using array element signal intensities alone, this local mean normalization process can correct for such artifacts because they vary across the surface of the array. The local mean normalization can be used for quality control and data correction purposes in the anal. of microarray data. These algorithms assume that array elements are not spatially ordered with regard to sequence or biol. function and require that this spatial mapping is identical between the two sets of intensities to be compared. The tool described in this report was developed in the R statistical language and is freely available on the Internet as part of a larger gene expression anal. package. This Web implementation is interactive and user-friendly and allows the easy use of the local mean normalization tool described here, without programming expertise or downloading of addnl. software.
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 287 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:403849 CAPLUS
DN 136:366101
TI Diagnostic microarray apparatus
IN Hammock, Bruce D.; Kido, Horacio; Maquieira, Angel
PA The Regents of the University of California, USA
SO U.S., 12 pp., Cont.-in-part of U.S. Ser. No. 64,387. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 6395562 B1 20020528 US 1998-148642 19980904 US 6342395 B1 20020129 US 1998-64387 19980422
PRAI US 1998-64387 A2 19980422

AB A compact assay system having a solid support has at least one capture binding agent on the support surface. By applying a combination of different binding agents on the support surface, the present invention can conduct multiple chem. reactions on the support solid support to detect analytes of interest. The specific reagents, or capture binding agents, are preferably immobilized on the solid support by means of a computer controlled, miniaturized printing system. Specifically, the reagents can be applied onto the solid support using a com. available printhead of an ink-jet printer. In addn., the support surface also includes areas adapted to be digitally readable by laser to store information concerning binding between capture agents and analytes. The assay system is useful as a sample array holder for performing a variety of chem. analyses, such as matrix assisted laser desorption ionization mass spectrometry analyses.
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 288 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:390357 CAPLUS
DN 137:273887
TI Identification of a novel cis-regulatory element involved in the heat shock response in Caenorhabditis elegans using microarray gene expression and computational methods
AU GuhaThakurta, Debraj; Palomar, Lisanne; Stormo, Gary D.; Tedesco, Pat; Johnson, Thomas E.; Walker, David W.; Lithgow, Gordon; Kim, Stuart; Link, Christopher D.
CS Department of Genetics, Washington University School of Medicine, St. Louis, MO, 63114, USA
SO Genome Research (2002), 12(5), 701-712 CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB We report here the identification of a previously unknown transcription regulatory element for heat shock (HS) genes in Caenorhabditis elegans. We monitored the expression pattern of 11,917 genes from C. elegans to det. the genes that were up-regulated on HS. Twenty eight genes were obsd. to be consistently up-regulated in several different repetitions of the expts. We analyzed the upstream regions of these genes using computational DNA pattern recognition methods. Two potential cis-regulatory motifs were identified in this way. One of these motifs (TTCTAGAA) was the DNA binding motif for the heat shock factor (HSF), whereas the other (GGGTGTC) was previously unreported in the literature. We detd. the significance of these motifs for the HS genes using different statistical tests and parameters. Comparative sequence anal. of orthologous HS genes from C. elegans and Caenorhabditis briggsae indicated that the identified DNA regulatory motifs are conserved across related species. The role of the identified DNA sites in regulation of HS genes was tested by in vitro mutagenesis of a green fluorescent protein (GFP) reporter transgene driven by the C. elegans hsp-16-2 promoter. DNA sites corresponding to both motifs are shown to play a significant role in up-regulation of the hsp-16-2 gene on HS. This is one of the rare instances in which a novel regulatory element, identified using computational methods, is shown to be biol. active. The contributions of individual sites toward induction of transcription on HS are nonadditive, which indicates interaction and cross-talk between the sites, possibly through the transcription factors (TFs) binding to these sites.
RE.CNT 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 289 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:387366 CAPLUS
DN 137:258032
TI Model-based analysis of oligonucleotide arrays
AU Li, Cheng
CS Univ. of California, Los Angeles, CA, USA
SO (2001) 97 pp. Avail.: UMI, Order No. DA3024060 From: Diss. Abstr. Int., B 2002, 62(8), 3679
DT Dissertation
LA English
AB Unavailable

L6 ANSWER 290 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:386251 CAPLUS
DN 137:17231
TI Exploring nature's plasticity with a flexible probing tool, and finding new ways for its electronic distribution
AU Beier, M.; Baum, M.; Rebscher, H.; Mauritz, R.; Wixmerten, A.; Stahler, C. F.; Muller, M.; Stahler, P. F.
CS Febit Ag, Mannheim, D-68167, Germany
SO Biochemical Society Transactions (2002), 30(2), 78-82 CODEN: BCSTB5; ISSN: 0300-5127
PB Portland Press Ltd.
DT Journal; General Review
LA English
AB A review. Concepts and results are described for the use of a single, but extremely flexible, probing tool to address a wide variety of genomic questions. This is achieved by transforming genomic questions into a software file that is used as the design scheme for potentially any genomic assay in a microarray format. Microarray fabrication takes place in three-dimensional microchannel reaction carriers by in situ synthesis based on spatial light modulation. This set-up allows for max. flexibility in design and realization of genomic assays. Flexibility is achieved at the mol., genomic and assay levels. We have applied this technol. to expression profiling and genotyping expts.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 291 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:376382 CAPLUS
DN 137:196212
TI Statistical methods for gene expression analysis from cDNA microarrays
AU Bryan, Jennifer Frazier
CS Univ. of California, Berkeley, CA, USA
SO (2001) 73 pp. Avail.: UMI, Order No. DA3019604 From: Diss. Abstr. Int., B 2002, 62(7), 3021
DT Dissertation
LA English
AB Unavailable

L6 ANSWER 292 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:358251 CAPLUS
DN 138:249687
TI Computational analysis of microarray gene expression profiles: clustering, classification, and beyond
AU Liang, Jie; Kachalo, Seman
CS Department of Bioengineering, University of Illinois at Chicago, Chicago, IL, 60607-7052, USA
SO Chemometrics and Intelligent Laboratory Systems (2002), 62(2), 199-216 CODEN: CILSEN; ISSN: 0169-7439
PB Elsevier Science B.V.
DT Journal
LA English
AB Gene array studies can assess the global expression patterns of thousands of genes under multiple conditions. This technol. can provide important insights about the underlying genetic causes of many important biol. questions, and can change our understanding of diseases, ultimately allowing the development of novel chem. entities as potential drug candidates. The informatics anal. and integration of gene expression pattern are crit. for interpreting gene array studies. In this paper, we discuss the computational anal. of three important tasks: (1) the identification of differentially expressed genes, (2) the discovery of gene clusters, and (3) the classification of biol. samples. In addn., we discuss how gene sequence and chem. structures can be profitably combined with microarray studies. Detailed examples are given throughout. Programs written in open source R language for achieving each of these tasks are freely available at gila.engr.uic.edu/genex.
RE.CNT 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 293 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:350223 CAPLUS
DN 138:85790
TI A dynamic spotting method for split-pin based microarrays
AU Zeng, Jun; Deshpande, Manish; Kan, Heng-Chuan; Gilbert, John R.
CS Coventor Inc., Cambridge, MA, 02138, USA
SO Micro Total Analysis Systems 2001, Proceedings .mu.TAS 2001 Symposium, 5th, Monterey, CA, United States, Oct. 21-25, 2001 (2001), 143-144. Editor(s): Ramsey, J. Michael; Berg, Albert van den. Publisher: Kluwer Academic Publishers, Dordrecht, Neth. CODEN: 69COT6; ISBN: 1-4020-0148-7
DT Conference
LA English
AB The authors propose a non-contact spotting concept for split-pin based microarrays utilizing dynamic control of the trajectory of the split-pin. Numerical simulation demonstrates that this novel method not only avoids the necessity of the pin tip striking the surface of the substrate, but also offers a new mechanism to realize spot-vol.-on-demand, as well as enhance the uniformity of sample spots.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 294 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:332714 CAPLUS
DN 136:337373
TI Computer systems and methods for hierarchical cluster analysis of large sets of biological data including highly dense gene array data
IN Fahy, Eoin D.
PA USA
SO U.S. Pat. Appl. Publ., 21 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 2002052692	A1	20020502	US 1999-397380	19990915
PRAI US 1999-397380		19990915		

AB A system and corresponding method analyzes biol. data for sets of test subjects such as gene arrays of group test subjects into clusters and order the clusters into a hierarchy based on similarities and differences of biol. data corresponding to the test subjects. A combination of nonhierarchical clustering and hierarchical clustering methods is used to efficiently and effectively perform hierarchical clustering of such biol. data as highly dense gene arrays contg. many thousand test subjects such as genes. First the test subjects are nonhierarchically clustered according to similarities and differences of their biol. data as detd. by distance techniques. Representative values, such as mean values, of the biol. data are detd. for each nonhierarchical cluster of test subjects. These representative values are then used to hierarchically cluster the nonhierarchical clusters. Biol. data for each test subject is displayed in a row of a table. The rows of the table are arranged by the nonhierarchical clustering and further by the hierarchical clustering. Each value of the biol. data is color coded according to its value to display patterns in the hierarchically clustered biol. data.

L6 ANSWER 295 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:329270 CAPLUS
DN 136:321714
TI Method for the optimization of molecular multiplex diagnostics of tissue microarrays using Virtual Cell Nucleus Imaging
IN Cremer, Christoph; Kreth, Gregor
PA Ruprecht-Karls-Universitaet, Germany
SO Ger. Offen., 12 pp. CODEN: GWXXBX
DT Patent
LA German
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI DE 10052583 A1 20020502 DE 2000-10052583 20001023
PRAI DE 2000-10052583 20001023
AB The invention concerns the optimization of mol. multiplex diagnostics of tissue ***microarrays*** using Virtual Cell Nucleus Imaging (VIRNI); ***computer*** modeling is used to establish microscopic detectable marker locations in the cells. The method can be applied in tumor diagnosis.

L6 ANSWER 296 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:315135 CAPLUS
DN 136:305120
TI Detection of point mutations in DNA using ***microarrays*** of oligonucleotide probes and digital recognition by ***computer***
IN Jin, Dong Kyu
PA Cosmogenome Co., Ltd, S. Korea
SO PCT Int. Appl., 24 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2002033123 A1 20020425 WO 2000-KR1166 20001018 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG AU 2000079678 A5 20020429 AU 2000-79678 20001018
PRAI WO 2000-KR1166 A 20001018
AB The present invention relates to a digital DNA chip of oligonucleotides probes on a solid support for detecting point mutations in a DNA sample. The array is composed of a labeling part and a logic part. The labeling part of arrays includes catalog no., gene sequence no., ID no., command, and IP address (which indicates the information for sample DNA identification to be read by computer). Catalog no. represents the kind of chip constructed. Gene sequence no. reports the name of the gene with accession no. ID no. identifies the subject or patient being tested. Command directs a short message which shows urgent information. The genetic information is stored at the IP address. The labeling part may be constructed in the form of a bar code for digital recognition by computer. The logic part includes arrays of probes in 4 columns and at least 100 and up to a 100,000 rows. Each column consists of 2 symbols that include a control symbol (having detectable marker for digital recognition by computer) and a hybridization symbol. The hybridization symbol comprises oligonucleotide probes that are 5 to 30 nucleotides in length and that occupy known sites by substituting target oligonucleotide into A C G T in each column. A point mutation is present in the subject's DNA if both control and hybridization symbol are detected, whereas detection of only hybridization symbol indicates normal DNA. Thus, after hybridization the genetic information becomes apparent on the chip. Since the information is represented by discrete digital information, the information can be read and translated using a mech. device into digital information without analog to digital conversion. In another embodiment the device may be in the form of a CD-ROM for convenient recognition by computer. The information regarding the labeling and logic part may be stored by computer or transmitted to other researchers via the internet.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 297 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:297584 CAPLUS
DN 138:35505
TI Design and simulation of bi-directional microfluid driving systems
AU Jen, Chun-Ping; Lin, Yu-Cheng
CS Department of Engineering Science, National Cheng Kung University, Tainan, 701, Taiwan
SO Journal of Micromechanics and Microengineering (2002), 12(2), 115-121 CODEN: JMMIEZ; ISSN: 0960-1317
PB Institute of Physics Publishing
DT Journal
LA English
AB Micro total anal. systems (.mu.TAS) have been developed to perform a no. of anal. processes involving chem. reactions, sepn. and sensing on a single chip. In medical and biomedical applications, .mu.TAS must be designed considering special transport mechanisms to move samples and reagents through the microchannels in the system. For conventional micropumps, however, complicated relationships exist between the pumping mechanisms, the conditions under which the devices operate and the behavior of the multi-component fluids transported in these channels. A bi-directional microfluid driving system has been developed in this paper. This pneumatic system is an on-chip planar structure with no moving parts and does not require microfabricated heaters or electrodes. The pumping actuation is introduced to the microchannel fabricated in the chip by blowing an airflow through this device. The bi-directional driving module combines two individual components for suction and exclusion. The driving system provides a stable and flexible bi-directional microfluid driving control. The tunable parameters for adjusting the exclusion/suction ratios, such as the location of the inlet channel and the velocities of the airflow, have been obsd. in the numerical study. The optimal exclusion/suction ratio for the specific purpose of the driving system can be selected by changing the location of the microchannel to the reaction area for the sample/reagent. The velocity at the microchannel can be adjusted by varying the inlet velocities for the suction and exclusion components. For the presented design, no air conduit was employed to connect the servo-system to the driving system; therefore the packaging difficulty and leakage problem, which may arise in conventional systems, can be eliminated. The final airflow outlet was fixed in one direction so that it can prevent cross-contamination between the servo-system and the chip. The driving system is therefore particularly suited to microdevices for biochem. anal. Diagrams describing the app. assembly and operation are given.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 298 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:296815 CAPLUS
DN 137:135674
TI OligoArray: genome-scale oligonucleotide design for microarrays
AU Rouillard, Jean-Marie; Herbert, Christopher J.; Zuker, Michael
CS Department of Chemical Engineering, University of Michigan, Ann Arbor, MI, 48109-2136, USA
SO Bioinformatics (2002), 18(3), 486-487 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB OligoArray is a program that computes gene specific and secondary structure free oligonucleotides for genome-scale oligonucleotide microarray construction or other applications.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 299 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:296804 CAPLUS
DN 136:366066
TI Analysis of matched mRNA measurements from two different microarray technologies
AU Kuo, Winston Patrick; Jenssen, Tor-Kristian; Butte, Atul J.; Ohno-Machado, Lucila; Kohane, Isaac S.
CS Children's Hospital Informatics Program and Division of Endocrinology, Department of Medicine, Children's Hospital, Decision Systems Group, Harvard Medical School, Brigham and Women's Hospital, Boston, MA, 02115, USA
SO Bioinformatics (2002), 18(3), 405-412 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Motivation: The existence of several technologies for measuring gene expression makes the question of cross-technol. agreement of measurements an important issue. Cross-platform utilization of data from different technologies has the potential to reduce the need to duplicate expts. but requires corresponding measurements to be comparable. Methods: A comparison of mRNA measurements of 2895 sequence-matched genes in 56 cell lines from the std. panel of 60 cancer cell lines from the National Cancer Institute (NCI 60) was carried out by calcg. correlation between matched measurements and calcg. concordance between cluster from two high-throughput DNA microarray technologies, Stanford type cDNA microarrays and Affymetrix oligonucleotide microarrays. Results: In general, corresponding measurements from the two platforms showed poor correlation. Clusters of genes and cell lines were discordant between the two technologies, suggesting that relative intra-technol. relationships were not preserved. GC-content, sequence length, av. signal intensity, and an estimator of cross-hybridization were found to be assocd. with the degree of correlation. This suggests gene-specific, or more correctly probe-specific, factors influencing measurements differently in the two platforms, implying a poor prognosis for a broad utilization of gene expression measurements across platforms.
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 300 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:265317 CAPLUS
DN 136:278873
TI Diagnosis support system using databases of DNA microarray gene expression patterns, disease association, and genetic information
IN Saito, Satoshi; Mitsuyama, Satoshi; Matsuo, Hitoshi; Hashiguchi, Takeshi
PA Hitachi Ltd., Japan
SO Jpn. Kokai Tokkyo Koho, 6 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI JP 2002107366 A2 20020410 JP 2000-306622 20001002
PRAI JP 2000-306622 20001002
AB A computer based system for supporting the diagnosis of current or future diseases is disclosed. A database of DNA microarray results for gene expression patterns is compared with disease assocn. database to predict diseases likely to occur, and DNA microarray database is compared to genetic information database to update

the disease assocn. database. The genetic information database contains information about the patients' family background, clin. results, life styles, and prescription, etc.

L6 ANSWER 301 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:243004 CAPLUS
DN 137:242587
TI Model-based cluster analysis of microarray gene-expression data
AU Pan, Wei; Lin, Jizhen; Le, Chap T.
CS Division of Biostatistics, School of Public Health, University of Minnesota, Minneapolis, MN, 55455-0378, USA
SO GenomeBiology [online computer file] (2002), 3(2), No pp. give CODEN: GNBLFW; ISSN: 1465-6914 URL: http://genomebiology.com/2002/3/2/research/0009
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Background: Microarray technologies are emerging as a promising tool for genomic studies. The challenge now is how to analyze the resulting large amts. of data. Clustering techniques have been widely applied in analyzing microarray gene-expression data. However, normal mixt. model-based cluster anal. has not been widely used for such data, although it has a solid probabilistic foundation. Here, we introduce and illustrate its use in detecting differentially expressed genes. In particular, we do not cluster gene-expression patterns but a summary statistic, the t-statistic. Results: The method is applied to a data set contg. expression levels of 1176 genes of rats with and without pneumococcal middle-ear infection. Three clusters were found, two of which contain more than 95% genes with almost no altered gene-expression levels, whereas the third one has 30 genes with more or less differential gene-expression levels. Conclusions: Our results indicate that model-based clustering of t-statistics (and possibly other summary statistics) can be a useful statistical tool to exploit differential gene expression for microarray data.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 302 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:232223 CAPLUS
DN 137:211508
TI Cluster-Rasch models for microarray gene expression data
AU Li, Hongzhe; Hong, Fangxin
CS Departments of Medicine and Statistics, University of California, Davis, CA, 95616, USA
SO GenomeBiology [online computer file] (2001), 2(8), No pp. given CODEN: GNBLFW; ISSN: 1465-6914 URL: http://genomebiology.com/2001/2/8/research/0031
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Background: We propose two different formulations of the Rasch statistical models to the problem of relating gene expression profiles to the phenotypes. One formulation allows us to investigate whether a cluster of genes with similar expression profiles is related to the obsd. phenotypes; this model can also be used for future prediction. The other formulation provides an alternative way of identifying genes that are over- or underexpressed from their expression levels in tissue or cell samples of a given tissue or cell type. Results: We illustrate the methods on available datasets of a classification of acute leukemias and of 60 cancer cell lines. For tumor classification, the results are comparable to those previously obtained. For the cancer cell lines dataset, we found four clusters of genes that are related to drug response for many of the 90 drugs that we considered. In addn., for each type of cell line, we identified genes that are over- or underexpressed relative to other genes. Conclusions: The cluster-Rasch model provides a probabilistic model for describing gene expression patterns across samples and can be used to relate gene expression profiles to phenotypes.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 303 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:226439 CAPLUS
DN 137:104339
TI Improved background correction for spotted DNA microarrays
AU Kooperberg, Charles; Fazzio, Thomas G.; Delrow, Jeffrey J.; Tsukiyama, Toshio
CS Division of Public Health Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA, 98109-1024, USA
SO Journal of Computational Biology (2002), 9(1), 55-66 CODEN: JCOBEM; ISSN: 1066-5277
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB Most microarray scanning software for glass spotted arrays provides ests. for the intensity for the "foreground" and "background" of two channels for every spot. The common approach in further analyzing such data is to first subtract the background from the foreground for each channel and to use the ratio of these two results as the est. of the expression level. The resulting ratios are, after possible averaging over replicates, the usual inputs for further data anal., such as clustering. If, with this background correction procedure, the foreground intensity was smaller than the background intensity for a channel, that spot (on that array) yields no usable data. In this paper it is argued that this preprocessing leads to ests. of the expression that have a much larger variance than needed when the expression levels are low.
RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 304 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:224142 CAPLUS
DN 137:226986
TI Mining mouse microarray data
AU Wigle, Dennis A.; Rossant, Janet; Jurisica, Igor
CS Dep. Medical Genetics Microbiology, Univ. Toronto, Toronto, ON, M5S 1A8, Can.
SO GenomeBiology [online computer file] (2001), 2(7), No pp. given CODEN: GNBLFW; ISSN: 1465-6914
PB BioMed Central Ltd.
DT Journal; General Review; (online computer file)
LA English
AB A review. Microarrays of mouse genes are now available from several sources, and they have so far given new insights into gene expression in embryonic development, regions of the brain and during apoptosis. Microarray data posted on the internet can be reanalyzed to study a range of question.
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 305 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:213437 CAPLUS
DN 137:211489
TI CGO: utilizing and integrating gene expression microarray data in clinical research and data management
AU Bumm, Klaus; Zheng, Mingzhong; Bailey, Clyde; Zhan, Fenghuang; Chiriva-Internati, M.; Eddlemon, Paul; Terry, Julian; Barlogie, Bart; Shaughnessy, John D., Jr.
CS Donna D. and Donald M. Lambert Laboratory of Myeloma Genetics and Myeloma, University of Arkansas for Medical Sciences, Little Rock, AR, 72205, USA
SO Bioinformatics (2002), 18(2), 327-328 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Clin. GeneOrganizer (CGO) is a novel windows-based archiving, organization and data mining software for the integration of gene expression profiling in clin. medicine. The program implements various user-friendly tools and exts. data for further statistical anal. This software was written for Affymetrix GeneChip *.txt files, but can also be used for any other microarray-derived data. The MS-SQL server version acts as a data mart and links microarray data with clin. parameters of any other existing database and therefore represents a valuable tool for combining gene expression anal. and clin. disease characteristics.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 306 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:213435 CAPLUS
DN 137:211487
TI DRAGON view: information visualization for annotated microarray data
AU Bouton, Christopher M. L. S.; Pevsner, Jonathan
CS Department of Neuroscience, Johns Hopkins School of Medicine, Baltimore, MD, 21205, USA
SO Bioinformatics (2002), 18(2), 323-324 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB The DRAGON View information visualization tools aid in the comprehensive anal. of large-scale gene expression data that has been annotated with biol. relevant information through the generation of three types of complementary graphical outputs.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 307 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:213428 CAPLUS
DN 137:211483
TI Mixture modelling of gene expression data from microarray experiments
AU Ghosh, Debashis; Chinnaiyan, Arul M.
CS Department of Biostatistics, University of Michigan, Ann Arbor, MI, 48109-2029, USA
SO Bioinformatics (2002), 18(2), 275-286 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Motivation: Hierarchical clustering is one of the major anal. tools for gene expression data from microarray expts. A major problem in the interpretation of the output from these procedures is assessing the reliability of the clustering results. We address this issue by developing a mixt. model-based approach for the anal. of microarray data. Within this framework, we present novel algorithms for clustering genes and samples. One of the byproducts of our method is a probabilistic measure for the no. of true clusters in the data. Results: The proposed methods are illustrated by application to microarray datasets from two cancer studies; one in which malignant melanoma is profiled, and the other in which prostate cancer is profiled.
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 308 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:213426 CAPLUS
DN 138:1890
TI Adjustments and measures of differential expression for microarray data
AU Tsodikov, A.; Szabo, A.; Jones, D.
CS Huntsman Cancer Institute and Department of Oncological Sciences, University of Utah, Salt Lake City, UT, 84112-5550, USA
SO Bioinformatics (2002), 18(2), 251-260 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal

LA English
AB Motivation: Existing analyses of microarray data often incorporate an obscure data normalization procedure applied prior to data anal. For example, ratios of microarray channels intensities are normalized to have common mean over the set of genes. We made an attempt to understand the meaning of such procedures from the modeling point of view, and to formulate the model assumptions that underlie them. Given a considerable diversity of data adjustment procedures, the question of their performance, comparison and ranking for various microarray expts. was of interest. Results: A two-step statistical procedure is proposed: data transformation (adjustment for slide-specific effect) followed by a statistical test applied to transformed data. Various methods of anal. for differential expression are compared using simulations and real data on colon cancer cell lines. We found that robust categorical adjustments outperform the ones based on a precisely defined stochastic model, including some commonly used procedures.
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 309 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:209098 CAPLUS
DN 137:211390
TI A DNA microarrays fabrication strategy for research laboratories
AU Tessier, Daniel C.; Thomas, David Y.; Brousseau, Roland
CS Montreal, Can.
SO Biotechnology (2nd Edition) (2001), Volume 5b, 227-237. Editor(s): Sensen, C. W. Publisher: Wiley-VCH Verlag GmbH, Weinheim, Germany. CODEN: 58AHA6
DT Conference; General Review
LA English
AB A review describing the practical implementation of a microarray facility using the fabrication of Candida albicans microarrays as an example. It is a feasible and cost-effective soln. for even small labs. to set up to produce their own high-quality microarrays for the genome of any species. The keys to this flexibility are the ability to synthesize large nos. of high-quality oligonucleotides in a cost-effective way and to have an integrated informatics platform to track samples and follow them through the quality control steps. Wider impact of microarray technol. is limited by the cost of the currently available microarrays and the relatively few species for which arrays are available.
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 310 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:207226 CAPLUS
DN 137:227073
TI Sources of nonlinearity in cDNA microarray expression measurements
AU Ramdas, Latha; Coombes, Kevin R.; Baggerly, Keith; Abruzzo, Lynne; Highsmith, W. Edward; Krogmann, Tammy; Hamilton, Stanley R.; Zhang, Wei
CS Departments of Pathology, Cancer Genomics Core Laboratory, University of Texas M D Anderson Cancer Center, Houston, TX, 77030, USA
SO GenomeBiology [online computer file] (2001), 2(11), No pp. given CODEN: GNBLFW; ISSN: 1465-6914 URL: http://www.genomebiology.com/2001/2/11/research/0047
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB A key assumption in the anal. of microarray data is that the quantified signal intensities are linearly related to the expression levels of the corresponding genes. To test this assumption, the authors exptl. examd. the relationship between signal and expression for the two types of microarrays they most commonly encounter: radioactively labeled cDNAs on nylon membranes and fluorescently labeled cDNAs on glass slides. Two sources of nonlinearity were recovered. The first, which led to discrepancies in anal. affecting the fluorescent signals, was signal quenching assocd. with excessive dye concns. The second, affecting the radioactive signals, was a nonlinear transformation of the raw data introduced by the scanner. Correction for this transformation was made by some, but not all, image-quantification software packages. The second type of nonlinearity is more troublesome, because it could not have been predicted a priori. Both types of nonlinearities were detected by simple diln. series, which the authors recommend as a quality-control step.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 311 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:200847 CAPLUS
DN 137:58216
TI Analysis of DNA microarrays using algorithms that employ rule-based expert knowledge
AU Pan, Kuang-Hung; Lih, Chih-Jian; Cohen, Stanley N.
CS Department of Genetics Program in Biomedical Informatics, Stanford University School of Medicine, and Department of Electrical Engineering, Stanford University, Stanford, CA, 94305-5120, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2002), 99(4), 2118-2123 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB The ability to investigate the transcription of thousands of genes concurrently by using DNA microarrays offers both major scientific opportunities and significant anal. challenges. Here we describe GABRIEL, a rule-based system of computer programs designed to apply domain-specific and procedural knowledge systematically and uniformly for the anal. and interpretation of data from DNA microarrays. GABRIEL's problem-solving rules direct stereotypical tasks, whereas domain-specific knowledge pertains to gene functions and relationships or to exptl. conditions. Addnl., GABRIEL can learn novel rules through genetic algorithms, which define patterns that best match the data being analyzed and can identify groupings in gene expression profiles preordered by chromosomal position or by a nonsupervised algorithm such as hierarchical clustering. GABRIEL subsystems explain the logic that underlies conclusions and provide a graphical interface and interactive platform for the acquisition of new knowledge. The present report compares GABRIEL's output with published findings in which expert knowledge has been applied post hoc to microarray groupings generated by hierarchical clustering.
RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 312 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:181080 CAPLUS
DN 136:275516
TI Carbohydrate microarrays for the recognition of cross-reactive molecular markers of microbes and host cells
AU Wang, Denong; Liu, Shaoyi; Trummer, Brian J.; Deng, Chao; Wang, Aili
CS Col;lege of Physicians and Surgeons, Columbia Genome Ctr., Columbia University, New York, NY, 10032, USA
SO Nature Biotechnology (2002), 20(3), 275-281 CODEN: NABIF9; ISSN: 1087-0156
PB Nature America Inc.
DT Journal
LA English
AB We describe here the development of a carbohydrate-based microarray to extend the scope of biomedical research on carbohydrate-mediated mol. recognition and anti-infection responses. We have demonstrated that microbial polysaccharides can be immobilized on a surface-modified glass slide without chem. conjugation. With this procedure, a large repertoire of microbial antigens (.apprx.20,000 spots) can be patterned on a single micro-glass slide, reaching the capacity to include most common pathogens. Glycoconjugates of different structural characteristics are shown here to be applicable for microarray fabrication, extending the repertoires of diversity and complexity of carbohydrate microarrays. The printed microarrays can be air-dired and stably stored at room temp. for long periods of time. In addn., the system is highly sensitive, allowing simultaneous detection of a broad spectrum of antibody specificities with as little as a few microliters of serum specimen. Finally, the potential of carbohydrate microarrays is demonstrated by the discovery of previously undescribed cellular markers, Dex-Ids.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 313 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:176383 CAPLUS
DN 136:211864
TI User authentication system, method and apparatus using DNA microarray, and its control method
IN Yamamoto, Nobuko; Ohno, Noriya
PA Canon Inc., Japan
SO Jpn. Kokai Tokkyo Koho, 11 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI JP 2002073572 A2 20020312 JP 2000-265689 20000901
PRAI JP 2000-265689 20000901
AB An user authentication system is provided, in which DNA is used for the user authentication in an electronic information exchange or an electronic trade, and thereby, the authentication is rapidly performed with high security. In this user authentication system for recognizing a normal user, an authentication card possessing a DNA microarray is used, on which the hybridization pattern is formed by reacting a DNA array with an user's DNA. The hybridization pattern is read from the DNA microarray of the authentication card by a scanner, and the information for an authentication registration or an authentication is sent to a computer at the contracter side. With the computer at the contracter side, the user registration is carried out according to the information transmitted, and the user authentication is performed by comparing the hybridization pattern shown by the transmitted information with the registered hybridization pattern.

L6 ANSWER 314 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:172524 CAPLUS
DN 136:211861
TI Method and system for predicting splice variant from DNA chip expression data
IN Wang, Yixin; Hu, Gang
PA USA
SO U.S. Pat. Appl. Publ., 15 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2002029113 A1 20020307 US 2001-934083 20010822
PRAI US 2000-226680P P 20000822
AB A system and method to predict alternative splicing transcripts using DNA chip expression data as a primary data source are disclosed. The system and method may perform prediction of alternative splicing of pre-mRNA that may be used, for example, for regulating eukaryotic gene expression.

L6 ANSWER 315 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:164142 CAPLUS
DN 136:275625

TI Contact Line Deposits on cDNA Microarrays: A "Twin-Spot Effect"
AU Blossey, Ralf; Bosio, Andreas
CS Fachbereich Physik, Universitaet Essen, Essen, D-45117, Germany
SO Langmuir (2002), 18(7), 2952-2954 CODEN: LANGD5; ISSN: 0743-7463
PB American Chemical Society
DT Journal
LA English
AB On the basis of CHG theory, we derive an equation for the radial distribution of the deposit concn. and discuss some of its properties. We give a simple criterion for the suppression of ring formation, applicable to the data of earlier expts. Second, we provide evidence for the convection-dominated deposit formation process by explaining a paradox of virtually identical deposits found.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 316 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:163704 CAPLUS
DN 137:196162
TI Genesis: cluster analysis of microarray data
AU Sturn, Alexander; Quackenbush, John; Trajanoski, Zlatko
CS Institute of Biomedical Engineering, Graz University of Technology, Graz, 8010, Austria
SO Bioinformatics (2002), 18(1), 207-208 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Summary: A versatile, platform independent and easy to use Java suite for large-scale gene expression anal. was developed. Genesis integrates various tools for microarray data anal. such as filters, normalization and visualization tools, distance measures as well as common clustering algorithms including hierarchical clustering, self-organizing maps, k-means, principal component anal., and support vector machines. The results of the clustering are transparent across all implemented methods and enable the anal. of the outcome of different algorithms and parameters. Addnl., mapping of gene expression data onto chromosomal sequences was implemented to enhance promoter anal. and investigation of transcriptional control mechanisms.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 317 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:163703 CAPLUS
DN 137:196161
TI CIT: identification of differentially expressed clusters of genes from microarray data
AU Rhodes, Daniel R.; Miller, Jeremy C.; Haab, Brian B.; Furge, Kyle A.
CS Laboratory of DNA and Protein Microarray Technology, Van Andel Research Institute, Grand Rapids, MI, 49053, USA
SO Bioinformatics (2002), 18(1), 205-206 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Summary: Cluster Identification Tool (CIT) is a microarray anal. program that identifies differentially expressed genes. Following division of exptl. samples based on a parameter of interest, CIT uses a statistical discrimination metric and permutation anal. to identify clusters of genes or individual genes that best differentiate between the exptl. groups. CIT integrates with the freely available CLUSTER and TREEVIEW programs to form a more complete microarray anal. package.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 318 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:154860 CAPLUS
DN 137:273570
TI Thresholding rules for recovering a sparse signal from microarray experiments
AU Sabatti, Chiara; Karsten, Stanislav L.; Geschwind, Daniel H.
CS Departments of Human Genetics and Statistics, and Department of Neurology, UCLA, Los Angeles, CA, 90095-7088, USA
SO Mathematical Biosciences (2002), 176(1), 17-34 CODEN: MABIAR; ISSN: 0025-5564
PB Elsevier Science Inc.
DT Journal
LA English
AB We consider array expts. that compare expression levels of a high no. of genes in two cell lines with few repetitions and with no subject effect. We develop a statistical model that illustrates under which assumptions thresholding is optimal in the anal. of such microarray data. The results of our model explain the success of the empirical rule of two-fold change. We illustrate a thresholding procedure that is adaptive to the noise level of the expt., the amt. of genes analyzed, and the amt. of genes that truly change expression level. This procedure, in a world of perfect knowledge on noise distribution, would allow reconstruction of a sparse signal, minimizing the false discovery rate. Given the amt. of information actually available, the thresholding rule described provides a reasonable estimator for the change in expression of any gene in two compared cell lines.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 319 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:147341 CAPLUS
DN 136:195281

TI Gene chips and computer system for obtaining genetic information necessary for prescription of genome medicine
IN Ueda, Yoshikatsu; Nosato, Kazuna; Kondo, Megumi
PA Hitachi Ltd., Japan
SO Jpn. Kokai Tokkyo Koho, 7 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI JP 2002058478 A2 20020226 JP 2000-250533 20000822
PRAI JP 2000-250533 20000822
AB Gene chips contg. probes for obtaining genetic information necessary for prescription of genome medicine, are disclosed. Genetic information regarding the concurrent use of other drugs, adverse reactions, and pharmacol. efficacy, is obtained. Computer-based system and computer readable memory devices for inputing and analyzing hybridization patterns, are also claimed.

L6 ANSWER 320 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:142981 CAPLUS
DN 136:163688
TI Microarray detector and synthesizer
IN Sandstrom, Perry
PA Able Signal Company, LLC, USA
SO PCT Int. Appl., 77 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2002014838 A2 20020221 WO 2001-US41698 20010814 WO 2002014838 A3 20020606 WO 2002014838 C1 20020718 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG US 6567163 B1 20030520 US 2000-640617 20000817 US 6545758 B1 20030408 US 2000-679858 20001005 AU 2001087180 A5 20020225 AU 2001-87180 20010814 EP 1311828 A2 20030521 EP 2001-966691 20010814 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRAI US 2000-640617 A 20000817 US 2000-679858 A 20001005 WO 2001-US41698 W 20010814
AB The present invention relates to novel systems, devices, and methods comprising spatial light modulators for use in the reading and synthesis of microarrays. For example, the present invention provides micromirror systems for synthesizing and acquiring data from nucleic acid microarrays and systems for collecting, processing, and analyzing data obtained from a microarray.

L6 ANSWER 321 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:136715 CAPLUS
DN 137:42251
TI Fully automatic quantification of microarray image data
AU Jain, Ajay N.; Tokuyasu, Taku A.; Snijders, Antoine M.; Segraves, Richard; Albertson, Donna G.; Pinkel, Daniel
CS Comprehensive Cancer Center, Cancer Research Institute, and Department of Laboratory Medicine, University of California, San Francisco, CA, 94143, USA
SO Genome Research (2002), 12(2), 325-332 CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB .DNA microarrays are now widely used to measure expression levels and DNA copy no. in biol. samples. Ratios of relative abundance of nucleic acids are derived from images of regular arrays of spots contg. target genetic material to which fluorescently labeled samples are hybridized. Whereas there are a no. of methods in use for the quantification of images, many of the software systems in wide use either encourage or require extensive human interaction at the level of individual spots on arrays. We present a fully automatic system for microarray image quantification. The system automatically locates both subarray grids and individual spots, requiring no user identification of any image coordinates. Ratios are computed based on explicit segmentation of each spot. On a typical image of 6000 spots, the entire process takes less than 20 s. We present a quant. assessment of performance on multiple replicates of genome-wide array-based comparative genomic hybridization expts. By explicitly identifying the pixels in each spot, the system yields more accurate ests. of ratios than systems assuming spot circularity. The software, called UCSF Spot, runs on Windows platforms and is available free of charge for academic use.
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 322 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:136707 CAPLUS
DN 137:42250
TI High-throughput imaging of brain gene expression
AU Brown, Vanessa M.; Ossadtchi, Alex; Khan, Arshad H.; Cherry, Simon R.; Leahy, Richard M.; Smith, Desmond J.
CS Department of Molecular and Medical Pharmacology, Crump Institute for Molecular Imaging, School of Medicine, University of California, Los Angeles, CA, 90095, USA
SO Genome Research (2002), 12(2), 244-254 CODEN: GEREFS; ISSN: 1088-9051

PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB Voxelation is a new method for acquisition of three dimensional (3D) gene expression patterns in the brain. It employs high-throughput anal. of spatially registered voxels (cubes) to produce multiple volumetric maps of gene expression analogous to the images reconstructed in biomedical imaging systems. Using microarrays, 24 voxel images of coronal hemisections at the level of the hippocampus of both the normal human brain and Alzheimer's disease brain were acquired for 2000 genes. The anal. revealed a common network of coregulated genes, and allowed identification of putative control regions. In addn., singular value decompn. (SVD), a math. method used to provide economical explanations of complex data sets, produced images that distinguished between brain structures, including cortex, caudate, and hippocampus. The results suggest that voxelation will be a useful approach for understanding how the genome constructs the brain.
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 323 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:124216 CAPLUS
DN 137:42240
TI MarC-V: a spreadsheet-based tool for analysis, normalization, and visualization of single cDNA microarray experiments
AU Schageman, J. J.; Basit, M.; Gallardo, T. D.; Garner, H. R.; Shohet, R. V.
CS Southwestern Medical Center, The University of Texas, Dallas, TX, USA
SO BioTechniques (2002), 32(2), 338-340, 342, 344 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
AB The comprehensive anal. and visualization of data extd. from cDNA microarrays can be a time-consuming and error-prone process that becomes increasingly tedious with increased no. of gene elements on a particular microarray. With the increasingly large no. of gene elements on today's microarrays, anal. tools must be developed to meet this challenge. Here, the authors present MarC-V, a Microsoft Excel spreadsheet tool with Visual Basic macros to automate much of the visualization and calcn. involved in the anal. process while providing the familiarity and flexibility of Excel. Automated features of this tool include (i) lower-bound thresholding, (ii) data normalization, (iii) generation of ratio frequency distribution plots, (iv) generation of scatter plots color-coded by expression level, (v) ratio scoring based on intensity measurements, (vi) filtering of data based on expression level or specific gene interests, and (vii) exporting data for subsequent multi-array anal. MarC-V also has an importing function included for GenePix results (GPR) raw data files.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 324 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:124215 CAPLUS
DN 137:42239
TI Correcting for signal saturation errors in the analysis of microarray data
AU Hsiao, L.-L.; Jensen, R. V.; Yoshida, T.; Clark, K. E.; Blumenstock, J. E.; Gullans, S. R.
CS Harvard Medical School, Brigham and Women's Hospital, Boston, MA, USA
SO BioTechniques (2002), 32(2), 330-332, 334, 336 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
AB A variety of tech. errors have arisen in data anal. when using cDNA or oligonucleotide microarrays. One of the most insidious problems is the satn. of the hybridization signal of high-abundant transcripts. This problem arises from the truncation of the laser fluorescence signal. When the hybridization signal on the microarray is very strong, this truncation can result in serious consequences that may not be readily apparent to the user. As an illustration of this problem, two subclasses of normal human tissue samples (six liver and six lung samples) were analyzed with GeneChip probe arrays to evaluate the patterns of expression for approx. 7000 human genes. Five of these data sets were found to suffer from signal truncation. This caused several tissues to be incorrectly classified using hierarchical clustering. To rectify this problem so that the gene expression data could be properly compared and clustered, we developed a "filtering" procedure that identifies a subset of genes least affected by the signal satn. This filtering procedure can be obtained at www.hugeindex.org.
RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 325 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:123628 CAPLUS
DN 136:180174
TI Significance analysis of microarrays
IN Tusher, Virginia Goss; Tibshirani, Robert; Chu, Gilbert
PA USA
SO U.S. Pat. Appl. Publ., 22 pp., Cont.-in-part of U.S. Provisional Ser. No. 208,073. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE

PI US 2002019704 A1 20020214 US 2001-811762 20010319
WO 2001084139 A1 20011108 WO 2001-US14223 20010502
W: CA, JP
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR
PRAI US 2000-208073P P 20000504
US 2001-811762 A 20010319
AB Microarrays can measure the expression of thousands of genes and thus identify changes in expression between different biol. states. Methods are needed to det. the significance of these changes, while accounting for the enormous no. of genes. We describe a new method, Significance Anal. of Microarrays (SAM), that assigns a score to each gene based on the change in gene expression relative to the std. deviation of repeated measurements. For genes with scores greater than an adjustable threshold, SAM uses permutations of the repeated measurements to est. the percentage of such genes identified by chance, the false discovery rate (FDR). When the transcriptional response of human cells to ionizing radiation was measured by microarrays, SAM identified 34 genes that changed at least 1.5-fold with an estd. FDR of 12%, compared to FDRs of 60% and 84% using conventional methods of anal. Of the 34 genes, 19 were involved in cell cycle regulation, and 3 in apoptosis. Surprisingly, 4 nucleotide excision repair genes were induced, suggesting that this repair pathway for UV-damaged DNA might play a heretofore unrecognized role in repairing DNA damaged by ionizing radiation.

L6 ANSWER 326 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:111858 CAPLUS
DN 137:150667
TI Analysis of cDNA microarray images
AU Yang, Yee Hwa; Buckley, Michael J.; Speed, Terence P.
CS University of California, Berkeley, CA, 94720-3860, USA
SO Briefings in Bioinformatics (2001), 2(4), 341-349 CODEN: BBIMFX; ISSN: 1467-5463
PB Henry Stewart Publications
DT Journal; General Review
LA English
AB A review with refs. Microarrays are part of a new class of biotechnologies that allow the monitoring of expression levels for thousands of genes simultaneously. Image anal. is an important aspect of microarray expts., one that can have a potentially large impact on subsequent analyses, such as clustering or the identification of differentially expressed genes. This paper reviews a no. of existing image anal. methods used on cDNA microarray data. In particular, it describes and discusses the different segmentation and background adjustment methods. It was found that in some cases background adjustment can substantially reduce the precision - i.e., increase the variability of low-intensity spot values. In contrast, the choice of segmentation procedure seems to have a smaller impact.
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 327 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:74727 CAPLUS
DN 137:120104
TI From genome to proteome
AU Grus, F. H.; Augustin, A. J.; Pfeiffer, N.; Schmidt-Erfurth, U.
CS Universitats-Augenklinik, Mainz, 55101, Germany
SO Ophthalmologe (2001), 98(12), 1132-1137 CODEN: OHTHEJ; ISSN: 0941-293X
PB Springer-Verlag
DT Journal; General Review
LA German
AB A review on application of DNA microarrays in simultaneous investigation of diverse disease-assocd. gene expressions. Proteome anal., 2-dimensional gel electrophoresis of tear protein patterns of diabetic patients and patients with Sicca syndrome, and data evaluation by bioinformatics using neuronal networks are described.
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 328 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:51674 CAPLUS
DN 136:97275
TI Manipulation of hybridizations of gene expression ***microarray*** by ***computer*** -implemented method
IN Gupta, Robert P.; Choi, Kirindi V. M.; Brahms, Robert A.; Chang, Doris; Chong, Darryl V. K.; Burrill, John D.; Marcus, Gregory; Bartha, Gabor T.; Head, Richard
PA Incyte Genomics, Inc., USA
SO PCT Int. Appl., 30 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE

PI WO 2002004676 A2 20020117 WO 2001-US21382 20010705
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG US 6424921 B1 20020723 US 2000-613167 20000710 US 2002188409 A1 20021212 US 2002-199239 20020719
PRAI US 2000-613167 A 20000710
AB The invention relates to computer-implemented method of averaging a plurality of hybridization of gene expression microarray. Composite hybridization arrays and averaged hybridization arrays are provided. Composite hybridization arrays are formed

a user selected set of hybridization arrays, and once instantiated in a hybridization array database, are available for searching, anal., and other data processing as with other types of hybridization arrays. This allows otherwise expts. using multiple different nucleotide microarrays to be efficiently consolidated and analyzed. Averaged hybridization array provide correctly averaged values from multiple user selected dual channel hybridization arrays.

L6 ANSWER 329 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:51340 CAPLUS
DN 136:66601
TI Microarray dispensing with real-time verification and inspection
IN Ganz, Brian L.; Mickley, Mandel W.; Moulds, John Andrew; Brovold, Christopher T.
PA Robodesign International, Inc., USA
SO PCT Int. Appl., 67 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 3 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2002004123 A1 20020117 WO 2001-US21223 20010705 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG US 6558623 B1 20030506 US 2000-611256 20000706 EP 1307291 A1 20030507 EP 2001-950868 20010705 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRAI US 2000-611256 A 20000706 WO 2001-US21223 W 20010705
AB A microarrayer for spotting soln. onto slides (4A-4E) in an automated microarray dispensing device. Elements of the present in vetion include: at least one dispense head (6) for spotting the slides, at least one light source (13) capable of illuminating the slides, at least one camera (12) operating in conjunction with the at least one light source. The at least one camera capable of acquiring and transmitting slide image data to a computer. The computer (300) is programmed to receive the slide image data and analyze it. The computer will then generate post anal. data based on the anal. of the slide image data. The post anal. data is available for improving the spotting of the soln. onto the slides. In a preferred embodiment, the slide image data includesidentification information. In a preferred embodiment, the anal. of the information relating to slide alignment enables the computer to make automatic adjustments to the relative positions of the at least one dispense head and the slides to increase the accuracy of the spotting. In a preferred embodiment, the anal. of the information relating to spot quality identifies a spot as pass or fail. An operator is then able to rework the spot. In a preferred embodiment, the anal. of the slide identification information enables the computer to track each slide.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 330 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:14225 CAPLUS
DN 136:130970
TI DNA word design strategy for creating sets of non-interacting oligonucleotides for DNA microarrays
AU Li, Ming; Lee, Hye Jin; Condon, Anne E.; Corn, Robert M.
CS Department of Chemistry, University of Wisconsin-Madison, Madison, WI, 53706, USA
SO Langmuir (2002), 18(3), 805-812 CODEN: LANGD5; ISSN: 0743-7463
PB American Chemical Society
DT Journal
LA English
AB A template-map design strategy for generating sets of non-interacting DNA oligonucleotides for applications in DNA arrays and biosensors is demonstrated. This strategy is used to create a set of oligonucleotides of size with length l that possess at least n base mismatches with the complements of all the other members in the set. These "DNA word" sets are denoted as nbm l-mers or l:n sets. To regularize the thermodn. stability of the perfectly matched hybridized DNA duplexes, the l-mers chosen for all the sets are required to have an approx. 50% G/C content. To achieve good discrimination between each DNA word in each set generated using the template-map strategy, it is required that n should be approx. equal to l/2 or higher. The template-map strategy can be used in a straightforward manner to create DNA word sets for cases when l = 4k and n = 2k, where k is an integer. Specific examples of 4k:2k sets are designed: an 8:4 set (s = 224), a 12:6 set (s = 528), a 16:8 set (s = 960), and a 20:10 set (s = 1520). These sets are further optimized to achieve the narrowest possible distribution of melting temps. by selecting the best set after permutation of the templates and maps over all possible configurations. To demonstrate the viability of this methodol., a non-interacting set of four specific 6bm 12mers have been chosen, synthesized, and used in an SPR imaging measurement of the hybridization adsorption onto a DNA array. The template-map strategy is also applied to generate DNA word sets for cases where l .noteq. 4k. In these cases, the creation of the maps and templates is more complicated, but possible. The templates and maps for three addnl. types of sets are created: (4k - 1):(2k - 1), (4k + 1):2k, and (4k - 2):(2k - 1). Specific examples are given for l = 7, 9, and 10: DNA word sets of 7:3 (s = 224), 9:4 (s = 360), and 10:5 (s = 132).
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 331 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:10825 CAPLUS
DN 136:50683
TI Method and computer programs for processing gene expression data obtained from DNA chip hybridization
IN Konishi, Tomokazu
PA Japan
SO PCT Int. Appl., 48 pp. CODEN: PIXXD2
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2002001477 A1 20020103 WO 2001-JP4697 20010604 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG EP 1313055 A1 20030521 EP 2001-934523 20010604 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR US 2003182066 A1 20030925 US 2002-311691 20021219
PRAI JP 2000-193680 A 20000628 JP 2001-24990 A 20010201
WO 2001-JP4697 W 20010604
AB A method and computer programs for processing gene expression data obtained from DNA chip hybridization, are disclosed. It involves the steps of logarithmic conversion, detn. of median value, z-normalization, for computing a background value. Chi square anal. is also used. A background computing unit of an anal. device computes such a background value such that a normal probability graph based on a cumulative frequency ratio of a subtracted value obtained by subtracting a background value from the individual values indicating the signal intensities of spots arranged on a DNA chip may have a predetd. linearity. A logarithmic conversion value of a cor. signal intensity value, as prepd. by subtracting the background value from the values indicating the signal intensities, takes the form of a normal distribution. By standardizing the normal distribution, therefore, it is possible to compare the data which are measured from the DNA chips of the same kind or of different kinds.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 332 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:929542 CAPLUS
DN 136:142204
TI Selective MOVPE of microarray waveguide for densely integrated photonic devices
AU Sudo, Shinya; Kudo, Koji; Mori, Kazuo; Sasaki, Tatsuya
CS Photonic and Wireless Devices Research Laboratories, System Devices and Fundamental Research, NEC Corporation, Otsu, 520-0833, Japan
SO Conference Proceedings - International Conference on Indium Phosphide and Related Materials, 13th, Nara, Japan, May 14-18, 2001 (2001), 390-393 Publisher: Institute of Electrical and Electronics Engineers, New York, N. Y. CODEN: 69CCW7
DT Conference
LA English
AB The authors studied the mask interference effect in selective OMVPE of a microarray optical waveguide. The authors studied the characteristics of waveguides having mask interference effects. Based on the exptl. results, the authors developed a method of ***simulating*** the characteristics of a ***microarray*** waveguide that uses the mask interference const., which depends on growth pressure. The simulation can account for the exptl. results under different growth pressures and it should be very useful for designing the microarray waveguides. In particular, the authors can use it to control the PL-wavelength profile of the microarray waveguide grown under atm. pressure, which is important for fabricating densely integrated photonic devices.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 333 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:926718 CAPLUS
DN 137:90354
TI A design method of DNA chips for SNP analysis using self organizing maps
AU Douzono, Hiroshi; Hara, Shigeomi; Noguchi, Yoshio
CS Faculty of Science and Engineering Saga University, Saga, 840-8502, Japan
SO International Joint Conference on Neural Networks, Proceedings, Washington, DC, United States, July 15-19, 2001 (2001), Volume 4, 2467-2471 Publisher: Institute of Electrical and Electronics Engineers, New York, N. Y. CODEN: 69CDDP
DT Conference
LA English
AB In this paper, we introduce a design method of DNA chips using Self-Organizing Maps(SOM). DNA chips are powerful tools for sequencings and SNP (Single Nucleotide Polymorphism) analyses of DNA sequences. A DNA chip is an array of DNA probes which are hybridized with the compliment sub-sequences in the target sequence. However, conventional DNA chips are showing tendency to be comprised of longer probes and get larger in size to achieve a higher resoln. To shrink the size of DNA chips, the design is considered to be important. To solve this problem, we applied SOM to obtain common features of DNA sequences with small no. of probes which efficiently cover the target sequence with sufficient resoln. for finding the correct position of SNPs. We evaluated the DNA chips designed by SOM with computer simulations of SNP analyses changing the length of probes and size of the maps.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 334 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:925409 CAPLUS
DN 136:364380
TI Assessing gene significance from cDNA microarray expression data via mixed models
AU Wolfinger, Russell D.; Gibson, Greg; Wolfinger, Elizabeth D.; Bennett, Lee; Hamadeh, Hisham; Bushel, Pierre; Afshari, Cynthia; Paules, Richard S.
CS SAS Institute Inc., Cary, NC, 27513, USA
SO Journal of Computational Biology (2001), 8(6), 625-637 CODEN: JCOBEM; ISSN: 1066-5277
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB The detn. of a list of differentially expressed genes is a basic objective in many cDNA microarray expts. We present a statistical approach that allows direct control over the percentage of false positives in such a list and, under certain reasonable assumptions, improves on existing methods with respect to the percentage of false negatives. The method accommodates a wide variety of exptl. designs and can simultaneously assess significant differences between multiple types of biol. samples. Two interconnected mixed linear models are central to the method and provide a flexible means to properly account for variability both across and within genes. The mixed model also provides a convenient framework for evaluating the statistical power of any particular exptl. design and thus enables a researcher to a priori select an appropriate no. of replicates. We also suggest some basic graphics for visualizing lists of significant genes. Analyses of published expts. studying human cancer and yeast cells illustrate the results.
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 335 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:924037 CAPLUS
DN 136:49310
TI DNA microarray assay for genetic polymorphisms using scattered light detectable labels
IN Bee, Gary; Kohne, David E.; Korb, Linda; Peterson, Todd; Yguerabide, Juan
PA Genicon Sciences Corporation, USA
SO PCT Int. Appl., 66 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2001096604 A2 20011220 WO 2001-US18912 20010611 WO 2001096604 A3 20030717 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG AU 2001075475 A5 20011224 AU 2001-75475 20010611 US 2002127561 A1 20020912 US 2001-880732 20010612
PRAI US 2000-210988P P 20000612 WO 2001-US18912 W 20010611
AB The invention provides a method for detg. the presence or absence of particular polymorphisms in CYP2D6 and other genes using scattered light detectable particles as detectable labels. The method utilizes a detection method based on the use of certain particles of specific compn., size, and shape and the detection and/or measurement of one or more of the particle's light scattering properties. The target sequences in a sample are bound to detectable light scattering particle, for example RLS (resonance light scattering) particle, which then illuminated with a light beam and the illumination can be detected by the human eye with less than 500 times magnification. Preferred RLS particles are composed of colloidal metals, preferably gold, silver, mixed gold and silver, or other mixed compn. particles contg. gold and or/silver. The invention provides convenient and sensitive detection for genetic polymorphisms, such as detection, insertion, and single nucleotide polymorphisms.

L6 ANSWER 336 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:904563 CAPLUS
DN 136:17715
TI Method and system for predicting nucleic acid hybridization thermodynamics and computer-readable storage medium for use therein
IN Santalucia, John, Jr.; Peyret, Nicolas
PA Wayne State University, USA
SO PCT Int. Appl., 100 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2001094611 A2 20011213 WO 2001-US18424 20010607 WO 2001094611 A3 20020418 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG AU 2001075349 A5 20011217 AU 2001-75349 20010607 EP 1311837 A2 20030521 EP 2001-942053 20010607 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR US 2003224357 A1 20031204 US 2001-876549 20010607
PRAI US 2000-209778P P 20000607 WO 2001-US18424 W 20010607
AB Method and system to predict and optimize probe-target hybridization are provided. The method may be implemented using six interactive, interrelated, software modules. Module 1 predicts the hybridization thermodn. of a duplex given the two strands. Module 2 finds the best primer of a given length binding to a given target. Module 3 executes a primer walk to find alternative binding sites of a given primer on a given target. Module 5 is a combination of Modules 2 and 3. Module 6 finds the alternative binding sites of a given primer on a given target (Module 3) and calcs. the concn. of target with primer bound at primary and alternative sites. Module 7 is a combination of Modules 2 and 5 and also calcs. the various concns. The six modules can be operated either through an interactive user interface or using batch file submission as provided by Module 4. The program is suited to predict DNA/DNA, RNA/RNA, and RNA/DNA systems.

L6 ANSWER 337 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:854745 CAPLUS
DN 137:73849
TI Gene expression profile analysis by DNA microarrays. Promise and pitfalls
AU King, Hadley C.; Sinha, Animesh A.
CS Dep. Dermatology, Weill Med. College, Cornell Univ., New York, NY, USA
SO JAMA, the Journal of the American Medical Association (2001), 286(18), 2280-2288 CODEN: JAMAAP; ISSN: 0098-7484
PB American Medical Association
DT Journal; General Review
LA English
AB A review with refs. DNA ***microarrays*** represent a technol. intersection between biol. and ***computers*** that enables gene expression anal. in human tissues on a genome-wide scale. This application can be expected to prove extremely valuable for the study of the genetic basis of complex diseases. Despite the enormous promise of this revolutionary technol., there are several issues and possible pitfalls that may undermine the authority of the microarray platform. We discuss some of the conceptual, practical, statistical, and logistical issues surrounding the use of microarrays for gene expression profiling. These issues include the imprecise definition of normal in expression comparisons; the cellular and subcellular heterogeneity of the tissues being studied; the difficulty in establishing the statistically valid comparability of arrays; the logistical logjam in anal., presentation, and archiving of the vast quantities of data generated; and the need for confirmational studies that address the functional relevance of findings. Although several complicated issues must be resolved, the potential payoff remains large.
RE.CNT 71 THERE ARE 71 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 338 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:832092 CAPLUS
DN 136:319942
TI High-throughput variation detection and genotyping using microarrays
AU Cutler, David J.; Zwick, Michael E.; Carrasquillo, Minerva M.; Yohn, Christopher T.; Tobin, Katherine P.; Kashuk, Carl; Mathews, Debra J.; Shah, Nila A.; Eichler, Evan E.; Warrington, Janet A.; Chakravarti, Aravinda
CS McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, Baltimore, MD, 21287, USA
SO Genome Research (2001), 11(11), 1913-1925 CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB The genetic dissection of complex traits may ultimately require a large no. of SNPs to be genotyped in multiple individuals who exhibit phenotypic variation in a trait of interest. Microarray technol. can enable rapid genotyping of variation specific to study samples. To facilitate their use, we have developed an automated statistical method (ABACUS) to analyze microarray hybridization data and applied this method to Affymetrix Variation Detection Arrays (VDAs). ABACUS provides a quality score to individual genotypes, allowing investigators to focus their attention on sites that give accurate information. We have applied ABACUS to an expt. encompassing 32 autosomal and eight X-linked genomic regions, each consisting of ~50 kb of unique sequence spanning a 100-kb region, in 40 humans. At sufficiently high-quality scores, we are able to read ~80% of all sites. To assess the accuracy of SNP detection, 108 of 108 SNPs have been exptl. confirmed; an addnl. 371 SNPs have been confirmed electronically. To access the accuracy of diploid genotypes at segregating autosomal sites, we confirmed 1515 of 1515 homozygous calls, and 420 of 423 (99.29%) heterozygotes. In replicate expts., consisting of independent amplification of identical samples followed by hybridization to distinct microarrays of the same design, genotyping is highly repeatable. In an autosomal replicate expt., 813,295 of 813,295 genotypes are called identically (including 351 heterozygotes); at an X-linked locus in males (haploid), 841,236 of 841,236 sites are called identically.
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 339 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:823845 CAPLUS
DN 137:1068
TI A statistical method for flagging weak spots improves normalization and ratio estimates in microarrays
AU Yang, M. C. K.; Ruan, Q. G.; Yang, J. J.; Eckenrode, S.; Wu, S.; McIndoe, R. A.; She, J. X.
CS Department of Statistics, University of Florida, Gainesville, FL, 32610-0275, USA

SO Physiological Genomics [online computer file] (2001), 7(1), 45-53 CODEN: PHGEFP; ISSN: 1094-8341 URL: http://physiolgenomics.physiology.org/cgi/reprint/7/1/45.pdf
PB American Physiological Society
DT Journal; (online computer file)
LA English
AB Over the last few years, there has been a dramatic increase in the use of cDNA microarrays to monitor gene expression changes in biol. systems. Data from these expts. are usually transformed into expression ratios between exptl. samples and a common ref. sample for subsequent data anal. The accuracy of this crit. transformation depends on two major parameters: the signal intensities and the normalization of the expt. vs. ref. signal intensities. A new model for microarray signal intensity that has one multiplicative variation and one additive background variation was described and validated. Using replicative expts. and simulated data, we found that the signal intensity is the most crit. parameter that influences the performance of normalization, accuracy of ratio ests., reproducibility, specificity, and sensitivity of microarray expts. Therefore, we developed a statistical procedure to flag spots with weak signal intensity based on the std. deviation (.delta.ij) of background differences between a spot and the neighboring spots, i.e., a spot is considered as too weak if the signal is weaker than c.delta.ij. Our studies suggest that normalization and ratio ests. were unacceptable when this threshold (c) is small. We further showed that when a reasonable compromise of c (c = 6) is applied, normalization using trimmed mean of log ratios performed slightly better than global intensity and mean of ratios. These studies suggest that decreasing the background noise is crit. to improve the quality of microarray expts.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 340 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:817051 CAPLUS
DN 135:341207
TI Statistical analysis of significance of microarray gene expression data
IN Tusher, Virginia Goss; Tibshirani, Robert; Chu, Gilbert
PA The Board of Trustees of the Leland Stanford Junior University, USA
SO PCT Int. Appl., 51 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2001084139 A1 20011108 WO 2001-US14223 20010502 W: CA, JP RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR US 2002019704 A1 20020214 US 2001-811762 20010319
PRAI US 2000-208073P P 20000504 US 2001-811762 A 20010319
AB Microarrays can measure the expression of thousands of genes and thus identify changes in expression between different biol. states. Methods are needed to det. the significance of these changes, while accounting for the enormous no. of genes. We describe a new method, Significance Anal. of Microarrays (SAM), that assigns a score to each gene based on the change in gene expression relative to the std. deviation of repeated measurements. For genes with scores greater than an adjustable threshold, SAM uses permutations of the repeated measurements to est. the percentage of such genes identified by chance, the false discovery rate (FDR). When the transcriptional response of human cells to ionizing radiation was measured by microarrays, SAM identified 34 genes that changed at least 1.5-fold with an estd. FDR of 12, compared to FDRs of 60 and 84 using conventional methods of anal. Of the 34 genes, 19 were involved in cell cycle regulation, and 3 in apoptosis. Surprisingly, 4 nucleotide excision repair genes were induced, suggesting that this repair pathway for UV-damaged DNA might play a heretofore unrecognized role in repairing DNA damaged by ionizing radiation.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 341 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:760998 CAPLUS
DN 136:380661
TI Construction of DNA microarray expression database and its data mining strategy
AU Kadota, Koji; Okazaki, Koji; Shimizu, Kentaro
CS Genomu Science Research Center, Institute of Physical and Chemical Research, Japan
SO Daikibo Genomu Kaiseki Gijutsu to Posuto Shikensu Jidai no Idenshi Kino Kaiseki (2001), 213-221. Editor(s): Shinagawa, Akira; Suzuki, Harukazu. Publisher: Nakayama Shoten, Tokyo, Japan. CODEN: 69BXSR
DT Conference; General Review
LA Japanese
AB A review. How to establish LIMS (Lab. Information Management Systems) for DNA array technologies and how to utilize the information in the database for data-mining were discussed. Image anal. softwares such as Scanalyze, ImaGene, QuantArray and ArrayAnalyzer and algorithms within for reading microarray results were described with a typical flow of the processing of DNA microarray results. The data-mining softwares such as Cluster, TreeView, Spotfire, Arrayscout and Genespring and how to ext. data from the microarray database and how to process the data were described. The procedures and tools for gene information annotation that would make cDNA database more valuable in data mining were also discussed with some actual examples of annotation systems such as FlyBase, NCBI and RIKEN definition.

L6 ANSWER 342 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:748048 CAPLUS
DN 135:283947
TI Cancer therapy patient classification based on microarray analysis of gene amplification or deletion using comparative genomic hybridization
IN Seelig, Steven A.
PA Vysis, Inc., USA
SO PCT Int. Appl., 61 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2001075160 A1 20011011 WO 2001-US10063 20010329 W: AU, CA, CN, JP, KR RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR CA 2402320 AA 20011011 CA 2001-2402320 20010329 EP 1268860 A1 20030102 EP 2001-964688 20010329 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR
PRAI US 2000-539400 A 20000331 WO 2001-US10063 W 20010329
AB The method of the invention comprises the classification of a cancer patient population into various cancer therapy groups based on anal. by genomic DNA microarray of multiple gene amplifications or deletions present or absent in the diseased tissue of each patient. In particular, the invention involves patient classification into one of at least four cancer therapy groups based on the microarray anal. of gene amplification or gene deletion at multiple chromosome locations. The invention has the significant clin. advantage of guiding selection of expensive cancer adjuvant drugs for use with patients most likely to respond pos. to the individual drug. For example, a genomic DNA microarray simultaneously measuring 59 sep. gene amplifications or gene deletions in diseased tissue can be used to stratify solid tumor cancer patients, such as breast cancer patients, into at least nine groups: those most likely to respond to (i) anti-HER-2/neu therapy (Herceptin), (ii) anti-EGFR therapy (C225 antibody), (iii) anti-AKT1 therapy (cis-platin), (iv) anti-PIK3CA therapy, (v) anti-thymidylate synthase therapy (5-fluorouracil), (iv) anti-Topoisomerase II therapy (doxorubicin), (vii) anti-cmyc therapy, (viii) combination of anti-HER-2 therapy and anti-AKT1 therapy, and (ix) combination of anti-EGFR and anti-AKT1 therapy. The invention has the significant clin. advantage of guiding selection of expensive cancer adjuvant drugs for use with patients most likely to respond pos. to the individual drug or respond synergistically to a particular combination of adjuvant therapies. The invention has yet another advantage, compared to use of nucleic acid microarrays measuring only gene expression changes in the diseased tissue from normal tissue, of measuring changes in a more stable analyte-chromosomal DNA, than the labile mRNA necessary for gene expression anal.
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 343 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:729488 CAPLUS
DN 136:366157
TI Metabolic context and possible physiological themes of .sigma.54-dependent genes in Escherichia coli
AU Reitzer, Larry; Schneider, Barbara L.
CS Department of Molecular and Cell Biology, The University of Texas at Dallas, Richardson, TX, 75083-0688, USA
SO Microbiology and Molecular Biology Reviews (2001), 65(3), 422-444 CODEN: MMBRF7; ISSN: 1092-2172
PB American Society for Microbiology
DT Journal; General Review
LA English
AB A review of .sigma.54-dependent genes in Escherichia coli. .sigma.54 Has several features that distinguish it from other sigma factors in Escherichia coli: it is not homologous to other .sigma. subunits, .sigma.54-dependent expression absolutely requires an activator, and the activator binding sites can be far from the transcription start site. A rationale for these properties has not been readily apparent, in part because of an inability to assign a common physiol. function for .sigma.54-dependent genes. Surveys of .sigma.54-dependent genes from a variety of organisms suggest that the products of these genes are often involved in nitrogen assimilation; however, many are not. Such broad surveys inevitably remove the .sigma.54-dependent genes from a potentially coherent metabolic context. To address this concern, we consider the function and metabolic context of .sigma.54-dependent genes primarily from a single organism, Escherichia coli, in which a reasonably complete list of .sigma.54-dependent genes has been identified by ***computer*** anal. combined with a DNA ***microarray*** anal. of nitrogen limitation-induced genes. E. coli appears to have approx. 30 .sigma.54-dependent operons, and about half are involved in nitrogen assimilation and metab. A possible physiol. relationship between .sigma.54-dependent genes may be based on the fact that nitrogen assimilation consumes energy and intermediates of central metab. The products of the .sigma.54-dependent genes that are not involved in nitrogen metab. may prevent depletion of metabolites and energy resources in certain environments or partially neutralize adverse conditions. Such a relationship may limit the no. of physiol. themes of .sigma.54-dependent genes within a single organism and may partially account for the unique features of .sigma.54 and .sigma.54-dependent gene expression.
RE.CNT 176 THERE ARE 176 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 344 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:715737 CAPLUS
DN 136:350826
TI DNA microarray gene expression analysis technology and its application to neurological disorders
AU Greenberg, Steven A.
CS Department of Neurology, Neuromuscular Division, Brigham and Women's Hospital, Boston, MA, 02115, USA
SO Neurology (2001), 57(5), 755-761 CODEN: NEURAI; ISSN: 0028-3878
PB Lippincott Williams & Wilkins
DT Journal; General Review

LA English
AB A review with refs. DNA ***microarray*** technol., also called "genechip" technol., it incorporates mol. genetics and ***computer*** science on a massive scale. This technol. can rapidly provide a detailed view of the simultaneous expression of entire genomes and provide new insights into gene function, disease pathophysiol., disease classification, and drug development. In this review, the author discusses the basic theory behind genechip and other biol. chip technologies, their limitations given the current state of biol. knowledge and computational abilities, and their potential applications to the understanding of neurol. disorders.
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 345 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:706675 CAPLUS
DN 136:5482
TI Query tools for microarray data mining applications
AU Groch, Kevin; Kuklin, Alexander
CS BioDiscovery, Inc., USA
SO PharmaGenomics (2001), (Aug.), 54-56 CODEN: PHARCV
PB Advanstar Communications, Inc.
DT Journal
LA English
AB A data mining package, called GeneSight, was developed to analyze quant. microarray data. It provides a no. of query tools and features for the desktop user to address both numerical and text-based needs. The package contains two specific tools designed to query a data set and assocd. textual information: the Template Matcher, for numerical queries into a data set, and the Query/Group Builder tool, for numerical queries into a data set, and the Query/Group Builder tool, for numerical and text-based queries into a data set as well as an underlying database contg. information about the genes present on a chip. In addn., this program contains several general features that aid the investigator in rapidly identifying specific genes based on their unique identifier within a data-set. The use of these tools and its specific features for exploring a modest-sized data set are described.
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 346 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:690367 CAPLUS
DN 135:223551
TI Comparative evaluation of laser-based microarray scanners
AU Ramdas, L.; Wang, J.; Hu, L.; Cogdell, D.; Taylor, E.; Zhang, W.
CS The University of Texas M. D. Cancer Center, Houston, TX, USA
SO BioTechniques (2001), 31(3), 546, 548, 550, 552 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
AB Labs. use different laser-based scanners to scan microarray images. To assess whether results from different scanners are comparable, and thus whether data from different labs. can be compared, we scanned the same microarray slide with three com. scanners that use different imaging techniques. After the acquisition of the microarray images produced by the three scanners, the images were quantified using a single imaging software package and protocol. The results were compared, and we found that the data obtained from the three scanners were comparable and that the variations caused by the use of different instruments were negligible, in spite of the fact that the scanners were based on different optical imaging techniques.
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 347 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:688156 CAPLUS
DN 136:66564
TI From split-pool libraries to spatially addressable microarrays and its application to functional proteomic profiling
AU Winssinger, Nicolas; Harris, Jennifer L.; Backes, Bradley J.; Schultz, Peter G.
CS Department of Chemistry and the Skaggs Institute for Chemical Biology, The Scripps Research Institute, La Jolla, CA, 92037, USA
SO Angewandte Chemie, International Edition (2001), 40(17), 3152-3155 CODEN: ACIEF5; ISSN: 1433-7851
PB Wiley-VCH Verlag GmbH
DT Journal
LA English
AB A method for the prepn. of small mol. microarrays using positionally encoded libraries and its application to functional proteomic profiling in a model system are presented. Libraries of small mols. tethered to peptidonucleic acid tags were constructed. The feasibility of this method was demonstrated using mechanism-based cysteine protease inhibitors contg. an acrylamide functionality. The PNA tag insignificantly affected the activity or selectivity of the inhibitor. A series of compds. designed to inhibit cathepsin S, L, H, B, C, and calpain were synthesized. Results showed that the proposed size exclusion sepn. is effective to sep. the bound PNA-ligand conjugates from the unbounding ones, and that PNA is efficient for positional encoding. Small mol.-PNA conjugates could be used to probe protein function in a microarray format. The ability to array small mol. libraries prepd. by split-pool combinatorial synthesis in a spatially addressable format allows for multiplexed screening in a highly miniaturized format to generate profiles of cellular activity.
RE.CNT 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 348 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:685169 CAPLUS
DN 136:336149
TI Simulator for gene expression networks
AU Armelin, Hugo A.; Barrera, Junior; Dougherty, Edward R.; Ferreira, Joao E.; Gubitoso, Marco D.; Hirata, Nina Sumiko Tomita; Neves, Eduardo J.
CS BIOINFO-USP, Nucleo de Pesquisa em Bioinformatica da Universidade de Sao Paulo, Sao Paulo, 05508-900, Brazil
SO Proceedings of SPIE-The International Society for Optical Engineering (2001), 4266(Microarrays: Optical Technologies and Informatics), 248-259 CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
AB This paper presents a simulator for gene expression networks, based on the model of chain dynamical systems (CDS). It gives the definition of CDS, describes the simulator architecture, the language adopted for describing CDS, and the available outputs. Finally, a real genetic network is studied: a subsystem of the genetic network that controls cell cycle of adrenocortical cells of the Y1 cultured cell line.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 349 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:685165 CAPLUS
DN 136:351319
TI Parallel computing methods for analyzing gene expression relationships
AU Suh, Edward B.; Dougherty, Edward R.; Kim, Seungchan; Russ, Daniel E.; Martino, Robert L.
CS Center for Information Technology, National Institutes of Health, Germantown, MD, 20892, USA
SO Proceedings of SPIE-The International Society for Optical Engineering (2001), 4266(Microarrays: Optical Technologies and Informatics), 213-221 CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
AB This paper presents a parallel program for assessing the codetn. of gene transcriptional states from large- scale simultaneous gene expression measurements with cDNA microarrays. The parallel program is based on a nonlinear statistical framework recently proposed for the anal. of gene interaction via multivariate expression arrays. Parallel computing is key in the application of the statistical framework to a large set of genes because a prohibitive amt. of computer time is required on a classical single-CPU machine. Our parallel program, named the Parallel Anal. of Gene Expression (PAGE) program, exploits inherent parallelism exhibited in the proposed codetn. prediction models. By running PAGE on 64 processors in Beowulf, a clustered parallel system, an anal. of melanoma cDNA ***microarray*** expression data has been completed within 12 days of ***computer*** time, an anal. that would have required about one and half years on a single-CPU computing system. A data visualization program, named the Visualization of Gene Expression (VOGE) program, has been developed to help interpret the massive amt. of quant. information produced by PAGE. VOGE provides graphical data visualization and anal. tools with filters, histograms, and accesses to other genetic databanks for further analyses of the quant. information.
RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 350 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:685161 CAPLUS
DN 136:306158
TI Random signal model for cDNA microarrays
AU Balagurunathan, Yoganand; Dougherty, Edward R.; Chen, Yidong; Bittner, Michael L.; Trent, Jeffrey M.
CS Department of Electrical Engineering, Texas A&M University, USA
SO Proceedings of SPIE-The International Society for Optical Engineering (2001), 4266(Microarrays: Optical Technologies and Informatics), 163-170 CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
AB The images resulting from cDNA microarrays are highly random. There are many aspects to this randomness, including spot size, shape, intensity, uniformity, and circularity, as well as both foreground and background noise. This paper presents a random model for the generation of microarray images. The model is complicated and contains over 20 parameters. It can be used to test ***microarray*** imaging algorithms and to ***simulate*** the effects of various dependencies within the image formation process.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 351 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:685151 CAPLUS
DN 136:351316
TI Rank-based algorithms for analysis of microarrays
AU Liu, Wei-min; Mei, Rui; Bartell, Daniel M.; Di, Xiaojun; Webster, Teresa A.; Ryder, Tom
CS Affymetrix, Inc., Santa Clara, CA, USA
SO Proceedings of SPIE-The International Society for Optical Engineering (2001), 4266(Microarrays: Optical Technologies and Informatics), 56-67 CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering

DT Journal
LA English
AB Anal. of microarray data often involves extg. information from raw intensities of spots of cells and making certain calls. Rank-based algorithms are powerful tools to provide probability values of hypothesis tests, esp. when the distribution of the intensities is unknown. For our current gene expression arrays, a gene is detected by a set of probe pairs consisting of perfect match and mismatch cells. The one-sided upper-tail Wilcoxon's signed rank test is used in our algorithms for abs. calls (whether a gene is detected or not), as well as comparative calls (whether a gene is increasing or decreasing or no significant change in a sample compared with another sample). We also test the possibility to use only perfect match cells to make calls. This paper focuses on abs. calls. We have developed error anal. methods and software tools that allow us to compare the accuracy of the calls in the presence or absence of mismatch cells at different target concns. The usage of nonparametric rank-based tests is not limited to abs. and comparative calls of gene expression chips. They can also be applied to other oligonucleotide microarrays for genotyping and mutation detection, as well as spotted arrays.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 352 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:685149 CAPLUS
DN 136:306322
TI Groundtruth approach to accurate quantitation of fluorescence microarrays
AU Kegelmeyer, Laura Mascio; Tomascik-Cheeseman, Lisa; Burnett, Melinda S.; van Hummelen, Paul; Wyrobek, Andrew J.
CS Lawrence Livermore National Laboratory, Livermore, CA, 94550, USA
SO Proceedings of SPIE-The International Society for Optical Engineering (2001), 4266(Microarrays: Optical Technologies and Informatics), 35-45 CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
AB To more accurately measure fluorescent signals from microarrays, we calibrated our acquisition and anal. systems by using groundtruth samples comprised of known quantities of red and green gene-specific DNA probes hybridized to cDNA targets. We imaged the slides with a full-field, white light CCD imager and analyzed them with our custom anal. software. Here we compare, for multiple genes, results obtained with and without preprocessing (alignment, color crosstalk compensation, dark field subtraction, and integration time). We also evaluate the accuracy of various image processing and anal. techniques (background subtraction, segmentation, quantitation and normalization). This methodol. calibrates and validates our system for accurate quant. measurement of microarrays. Specifically, we show that preprocessing the images produces results substantially closer to the known groundtruth for these samples.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 353 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:661548 CAPLUS
DN 135:207851
TI Microarray substrate with integrated photodetector and methods of use thereof
IN O'Keefe, Matthew T.
PA The Board of Trustees of the Leland Stanford Junior University, USA
SO PCT Int. Appl., 34 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
--- --- --- --- ---
PI WO 2001064831 A1 20010907 WO 2001-US6661 20010228 RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR US 2002004204 A1 20020110 US 2001-796932 20010228
PRAI US 2000-185878P P 20000229
AB The present invention provides a microarray substrate comprising a plurality of photodetectors integrated therein. The invention further provides a detection device for use in conjunction with a microarray substrate of the invention, as well as methods of use of same.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 354 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:656521 CAPLUS
DN 136:227437
TI Multiplex sequencing by hybridization
AU Hubbell, Earl
CS Department of Mathematics, University of Southern California, Los Angeles, CA, 90089-1113, USA
SO Journal of Computational Biology (2001), 8(2), 141-149 CODEN: JCOBEM; ISSN: 1066-5277
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB One of the limitations of classical sequencing by hybridization (SBH) is the inefficient use of probes in the "all k-mers" array. This limitation occurs due to the relatively short length (roughly C) of target that may be reconstructed by an array with C probes. We propose a new strategy, multiplex sequencing by hybridization, that greatly increases the efficiency of target reconstruction. In the typical multiplex SBH method, many different target sequences are simultaneously reconstructed (as compared to a single sequence in classic SBH). This is accomplished by pooling the target sequences and performing several hybridization expts. This procedure makes more efficient use of probes so that the combined length of sequence reconstructed per DNA array increases significantly as compared to classical SBH.
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 355 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:656515 CAPLUS
DN 136:227433
TI On differential variability of expression ratios: improving statistical inference about gene expression changes from microarray data
AU Newton, M. A.; Kendziorski, C. M.; Richmond, C. S.; Blattner, F. R.; Tsui, K. W.
CS Department of Statistics, University of Wisconsin, Madison, WI, 53792, USA
SO Journal of Computational Biology (2001), 8(1), 37-52 CODEN: JCOBEM; ISSN: 1066-5277
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB We consider the problem of inferring fold changes in gene expression from cDNA microarray data. Std. procedures focus on the ratio of measured fluorescent intensities at each spot on the microarray, but to do so is to ignore the fact that the variation of such ratios is not const. Ests. of gene expression changes are derived within a simple hierarchical model that accounts for measurement error and fluctuations in abs. gene expression levels. Significant gene expression changes are identified by deriving the posterior odds of change within a similar model. The methods are tested via ***simulation*** and are applied to a panel of Escherichia coli ***microarrays*** .
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 356 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:612422 CAPLUS
DN 135:238721
TI Surface-potential controlled Si-microarray devices for heterogeneous protein crystallization screening
AU Sanjoh, A.; Tsukihara, T.; Gorti, S.
CS Osaka University, Institute for Protein Research, Osaka, Suita, 565-0871, Japan
SO Journal of Crystal Growth (2001), 232(1-4), 618-628 CODEN: JCRGAE; ISSN: 0022-0248
PB Elsevier Science B.V.
DT Journal
LA English
AB Fundamental investigations of protein crystn. using microarrayed multiple cell Si-devices were proposed for achieving heterogeneous nucleation/crystn. and also for screening expts. Surface-potential (.zeta.-potential) controlled nucleation and crystn. sites made from deposited thin-film semiconductor and insulating materials were fabricated on the surface of each crystal growth cell. .zeta.-Potential measurement using the electrophoretic light scattering spectrophotometric method showed that both of ionic strength and pH values had a great influence on the potential of solid material surfaces, such as n/p-Si, SiO2, Si3N4, and Al2O3, and also protein ones. Isoelec. point of protein was influenced and shifted with the ionic strength, but point of zero charge of our solid material surface was still unchanged. Then the conventional microarrayed configuration was adopted in our device, but each unit well was composed of single reservoir and paired multiple crystal growth cells to prep. the protein droplets of different buffer and precipitant concns. The no. of our multiple growth cells in a unit well was at least 2, and the available vol. for protein drop ranged from 1 to 10 .mu.l. This cell configuration and sample prepn. was expected to cover the whole effective pH and concn. regions for heterogeneous nucleation and crystn. and accordingly accelerate the screening expts. without changing conventional reagents and protocols.
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 357 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:606406 CAPLUS
DN 136:363314
TI Searching for altered gene expression in arsenic sulfide treated K562 by DNA microarray
AU Gu, Chunhong; Chen, Fangyuan; Teng, Ye; Han, Jieying; Shao, Nianxian; Ouyang, Renrong
CS Department of Hematology, Renji Hospital, Shanghai Second Medical University, Shanghai, 200001, Peop. Rep. China
SO Shanghai Yixue (2001), 24(5), 263-265 CODEN: SIHSD8; ISSN: 0253-9934
PB Shanghai Yixue Bianji Weiyuanhui
DT Journal
LA Chinese
AB The altered gene expression of K562 cell after treatment with arsenic sulfide was detected by cDNA microarray. Two fluorescence cDNA probes were made from mRNA of arsenic sulfide untreated or treated K562 cells, marked with two different fluorescent dyes, cy3 or cy5 resp., hybridized with expressed cDNA ***microarray*** scanned and analyzed by ***computer*** system and finally detg. the altered expression of the gene. Eleven genes were identified, related to cell cycle, DNA transcription and transcription factors, and protein translation which were expressed differently after treatment with arsenic sulfide: 7/11 elevated, 4/11 depressed. It is suggested that cyclin E2, cyclin G2 may take part in the process of K562 cell apoptosis induced by arsenic sulfide.

L6 ANSWER 358 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:592717 CAPLUS
DN 135:300108
TI A study of DNA tethered to a surface by an all-atom molecular dynamics simulation
AU Wong, Ka-Yiu; Pettitt, B. Montgomery

CS Department of Chemistry and institute for Molecular Design, University of Houston, Houston, TX, 77204-5641, USA
SO Theoretical Chemistry Accounts (2001), 106(3), 233-235 CODEN: TCACFW; ISSN: 1432-881X
PB Springer-Verlag
DT Journal
LA English
AB In order to understand the structure of DNAs and their interactions when on ***microarray*** surfaces, we performed the first all-atom mol. dynamics ***simulation*** of DNA tethered to a surface. On the surface. the binding of the DNA was enhanced. and its av. equil. conformation was the B form. The DNA duplex spontaneously tilted towards its nearest neighbor and settled in a leaning position with a interaxial distance of 2.2 nm. This close packing of the DNAs, which affects both in situ synthesis and deposition of probes on microarray surfaces, can thus be explained by salted-induced colloidlike DNA-DNA attractions.
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 359 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:517338 CAPLUS
DN 135:256764
TI AMADA: analysis of microarray data
AU Xia, Xuhua; Xie, Zheng
CS Department of Ecology & Biodiversity, University of Hong Kong, Hong Kong, Hong Kong
SO Bioinformatics (2001), 17(6), 569-570 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB AMADA is a Windows program for identifying co-expressed genes from microarray data. It performs data transformation, principal component anal., a variety of cluster analyses and extensive graphic functions for visualizing expression profiles.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 360 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:517327 CAPLUS
DN 136:195244
TI A bayesian framework for the analysis of microarray expression data: regularized t-test and statistical inferences of gene changes
AU Baldi, Pierre; Long, Anthony D.
CS Department of Information and Computer Science, University of California at Irvine, Irvine, CA, 92697-3425, USA
SO Bioinformatics (2001), 17(6), 509-519 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB DNA microarrays are now capable of providing genome-wide patterns of gene expression across many different conditions. The first level of anal. of these patterns requires detg. whether obsd. differences in expression are significant or not. Current methods are unsatisfactory due to the lack of a systematic framework that can accommodate noise, variability, and low replication often typical of microarray data. A Bayesian probabilistic framework for microarray data anal. was developed. At the simplest level, we model log-expression values by independent normal distributions, parameterized by corresponding means and variances with hierarchical prior distributions. We derive point ests. for both parameters and hyperparameters, and regularized expressions for the variance of each gene by combining the empirical variance with a local background variance assocd. with neighboring genes. An addnl. hyperparameter, inversely related to the no. of empirical observations, dets. the strength of the background variance. Simulations show that these point ests., combined with a t-test, provide a systematic inference approach that compares favorably with simple t-test or fold methods, and partly compensate for the lack of replication.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 361 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:511792 CAPLUS
DN 135:241632
TI A comparison of microarray databases
AU Gardiner-Garden, Margaret; Littlejohn, Timothy G.
CS Entigen Pty Ltd., Eveleigh, 1430, Australia
SO Briefings in Bioinformatics (2001), 2(2), 143-158 CODEN: BBIMFX; ISSN: 1467-5463
PB Henry Stewart Publications
DT Journal
LA English
AB A survey and comparative anal. of microarray databases was undertaken in order to obtain a better understanding of the available systems. The survey included databases that are currently available, as well as databases that should become available in early 2001. Databases fall into three categories: those that can be installed locally, those available for public data submission, and those available for public query. Developers of microarray gene expression databases were asked questions regarding the scope and availability of their database, its system requirements, its future compliance with MGED (Microarray Gene Expression Database) stds., and its assocd. anal. tools. Each database fulfils a different role, reflecting the widely varying needs of microarray users.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 362 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:477188 CAPLUS
DN 136:178395
TI Predicting gene function from gene expressions and ontologies
AU Hvidsten, T. R.; Komorowski, J.; Sandvik, A. K.; Laegreid, A.
CS Knowledge Systems Group, Department of Information and Computer Science, Norwegian University of Science and Technology, Trondheim, 7491, Norway
SO Pacific Symposium on Biocomputing 2001, Mauna Lani, HI, United States, Jan. 3-7, 2001 (2001), 299-310. Editor(s): Altman, Russ B. Publisher: World Scientific Publishing Co. Pte. Ltd., Singapore, Singapore. CODEN: 69BLFC
DT Conference; General Review
LA English
AB A review. The authors introduce a methodol. for inducing predictive rule models for functional classification of gene expressions from microarray hybridization expts. The basic learning method is the rough set framework for rule induction. The methodol. is different from the commonly used unsupervised clustering approaches in that it exploits background knowledge of gene function in a supervised manner. Genes are annotated using Ashburner's Gene Ontol. and the functional classes used for learning are mined from these annotations. From the original expression data, we ext. a set of biol. meaningful features that are used for learning. A rule model is induced from the data described in terms of these features. Its predictive quality is fine-tuned via cross-validation on subsets of the known genes prior to classification of unknown genes. The predictive and descriptive quality of such a rule model is demonstrated on the fibroblast serum response data previously analyzed by V. R. Iyer et al. (1999). This anal. shows that the rules are capable of representing the complex relationship between gene expressions and function, and that it is possible to put forward high quality hypotheses about the function of unknown genes.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 363 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:468766 CAPLUS
DN 136:113358
TI Preprocessing implementation for microarray (PRIM): an efficient method for processing cDNA microarray data
AU Kadota, Koji; Miki, Rika; Bono, Hidemasa; Shimizu, Kentaro; Okazaki, Yasushi; Hayashizaki, Yoshihide
CS Labsoratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center, RIKEN Yokohama Institute, Yokohama City, Kanagawa, 230-0045, Japan
SO Physiological Genomics [online computer file] (2001), 4(3), 183-188 CODEN: PHGEFP; ISSN: 1094-8341 URL: http://physiolgenomics.physiology.org/cgi/reprint/4/3/183.pdf
PB American Physiological Society
DT Journal; (online computer file)
LA English
AB CDNA microarraytechnol. is useful for systematically analyzing the expression profiles of thousands of genes at once. Although many useful results inferred by using this technol. and a hierarchical clustering method for statistical anal. have been confirmed using other methods, there are still questions about the reproducibility of the data. We have therefore developed a data processing method that very efficiently exts. reproducible data from the result of duplicate expts. It is designed to automatically filter the raw results obtained from cDNA microarray image-anal. software. We optimize the threshold value for filtering the data by using the product of N and R, where N is the ratio of the no. of spots that passed the filtering vs. the total no. of spots, and R is the correlation coeff. for results obtained in the duplicate expts. Using this method to process mouse tissue expression profile data that contain 1,881,600 points of anal., we obtained clustered results more reasonable than those obtained using previously reported filtering methods.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 364 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:438179 CAPLUS
DN 136:146082
TI Analysis of temporal gene expression profiles: Clustering by simulated annealing and determining the optimal number of clusters
AU Lukashin, Alexander V.; Fuchs, Rainer
CS 14 Cambridge Center, Biogen Inc., Cambridge, MA, 02142, USA
SO Bioinformatics (2001), 17(5), 405-414 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Cluster anal. of genome-wide expression data from DNA microarray hybridization studies has proved to be a useful tool for identifying biol. relevant groupings of genes and samples. In the present paper, we focus on several important issues related to clustering algorithms that have not yet been fully studied. We describe a simple and robust algorithm for the clustering of temporal gene expression profiles that is based on the simulated annealing procedure. In general, this algorithm guarantees to eventually find the globally optimal distribution of genes over clusters. We introduce an iterative scheme that serves to evaluate quant. the optimal no. of clusters for each specific data set. The scheme is based on std. approaches used in regular statistical tests. The basic idea is to organize the search of the optimal no. of clusters simultaneously with the optimization of the distribution of genes over clusters. The efficiency of the proposed algorithm has been evaluated by means of a reverse engineering expt., i.e., a situation in which the correct distribution of genes over clusters is known a priori. The employment of this statistically rigorous test has shown that our algorithm places greater than 90% genes into correct clusters. Finally, the algorithm has been tested on real gene expression data (expression changes during

yeast cell cycle) for which the fundamental patterns of gene expression and the assignment of genes to clusters are well understood from numerous previous studies. The source code of the program implementing the algorithm is available upon request from the authors.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 365 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:360285 CAPLUS
DN 134:337911
TI Apparatus and method for using fiducial marks on a microarray substrate
IN Noblett, David
PA GSI Lumonics, Inc., USA
SO PCT Int. Appl., 26 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------
------ ---- -------- ---------- --------
PI WO 2001035099 A1 20010517 WO 2000-US28198 20001012 W:
CA, JP RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
PT, SE US 6362004 B1 20020326 US 1999-436974 19991109 CA
2390540 AA 20010517 CA 2000-2390540 20001012 EP 1228372
A1 20020807 EP 2000-970823 20001012 R: AT, BE, CH, DE, DK, ES, FR,
GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY
PRAI US 1999-436974 A 19991109 WO 2000-US28198 W 20001012
AB A microarray scanning system for conducting expts. on a planar substrate includes an app. for translating the secured substrate in two axes, the substrate having at least one fiducial mark on the planar substrate as a means for positioning and aligning the substrate for subsequent spot placement, anal., or comparison procedures.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 366 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:341257 CAPLUS
DN 135:76454
TI A system for finding association rules from microarray data and public databases
AU Naitou, Takahiro; Satou, Kenji; Furuichi, Emiko; Kuhara, Satoru; Takagi, Toshihisa
CS School of Knowledge Science, Japan Advanced Institute of Science and Technology, Ishikawa, 923-1292, Japan
SO Genome Informatics Series (2000), 11(Genome Informatics 2000), 356-357
CODEN: GINSE9; ISSN: 0919-9454
PB Universal Academy Press
DT Journal
LA English
AB As the research trend of genome anal. changes from sequencing to gene expression and genetic network identification, the microarray has attracted a great deal of attention. However, the methodol. for extg. knowledge from a set of microarray data is not yet established. Consequently, the clustering of genes according to their expressivity is still the most popular way for the first anal. to be tried. Since the data obtained from a microarray expt. consists solely of pairs of gene names and their expressivity, it is needed to combine this data with other information extd. from public databases in order to find useful knowledge. To solve this problem, a Web-based anal. system which can discovery assocn. rules from a combination of microarray data and public databases, is being developed. The functionalities of the prototype system currently under development, are described.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 367 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:341215 CAPLUS
DN 136:97204
TI Practical organization and functional annotation of RIKEN cDNA microarray
AU Bono, Hidemasa; Kasukawa, Takeya; Miki, Rika; Kadota, Koji; Okazaki, Yasushi; Hayashizaki, Yoshihide
CS Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, Kanagawa, 230-0045, Japan
SO Genome Informatics Series (2000), 11(Genome Informatics 2000), 260-261
CODEN: GINSE9; ISSN: 0919-9454
PB Universal Academy Press
DT Journal
LA English
AB An important issue in using DNA microarray technol. for analyzing gene expressions is the ability to predict gene functions from the similarity and dissimilarity of expression patterns. With this ability, the functional inference of genes that cannot be inferred from any sequence analyses can be readily obtained. However, this requires effective computational methods and resources. In this regard, a web-based system, called READ (Riken Expression Array Database), for analyzing cDNA microarray data from the RIKEN mouse 19K set is under development. The READ system organizes all the information that needs to be referred in the anal. phase, including the results of various sequence analyses.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 368 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:341205 CAPLUS
DN 135:76452
TI Data submission system for cyanobacterial DNA chip consortium
AU Uchiyama, Ikuo; Miwa, Tomoki; Nishide, Hiroyo; Suzuki, Iwane; Omata, Tatsuo; Ikeuchi, Masahiko; Murata, Norio; Kanehisa, Minoru
CS National Institute for Basic Biology, Research Center for Computational Science, Okazaki National Research Institutes, Okazaki, 444-8585, Japan
SO Genome Informatics Series (2000), 11(Genome Informatics 2000), 235-236
CODEN: GINSE9; ISSN: 0919-9454
PB Universal Academy Press
DT Journal
LA English
AB A DNA microarray is an extremely useful tool for functional genomics by surveying genome-wide gene expression changes in cells under different conditions. A cyanobacterial DNA chip consortium established under the Genome Frontier Project, consists of Japanese cyanobacterial researchers with a wide range of interests. In each member's lab., expts. are underway using the same chip on which segments of almost all ORFs identified in Synechocystis sp. PCC6803 genome are spotted, but using various materials subjected to changes in different environmental conditions such as temp., light intensity or CO2 concn. The data submission system for this consortium is hereby presented. The system accepts and manages data about exptl. conditions and relates them to the submitted expression data file produced from the image anal. software.
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 369 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:341199 CAPLUS
DN 136:1299
TI KEGG/EXPRESSION: a database for browsing and analyzing microarray expression data
AU Goto, Susumu; Kawashima, Shuichi; Okuji, Yoshinori; Kamiya, Tomomi; Miyazaki, Satoshi; Numata, Youjiro; Kanehisa, Minoru
CS Institute for Chemical Research, Kyoto University, Kyoto, 611-0011, Japan
SO Genome Informatics Series (2000), 11(Genome Informatics 2000), 222-223
CODEN: GINSE9; ISSN: 0919-9454
PB Universal Academy Press
DT Journal
LA English
AB A prototype of KEGG/EXPRESSION database was developed for storing publicly available yeast microarray data, which was used to analyze the aminoacyl-tRNA synthase behavior using the data. This database was integrated into the DBGET/LinkDB system, and new Java applets for browsing and analyzing the data were developed. Each entry of the KEGG/EXPRESSION in the DBGET/Link DB system corresponds to an array and contains the information on entry name, accession identification, brief description of the expt., conditions of the control and target arrays, experimenters, data and organism. This entry is in the HTML format and is a starting point to the browsing methods. The expression data from each expt. can be browsed as either a microarray image or a scatter plot. Three types of plots are available, a plot for whole genes, classified plots according to the KEGG functional classification, and classified plots according to the functional classification by the sequencing group of the organism. This database also links to various anal. tools from the result of the browser and the list of genes.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 370 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:335897 CAPLUS
DN 135:71709
TI ***Microarray*** analysis of genes differentially expressed in HepG2 cells cultured in ***simulated*** microgravity: Preliminary report
AU Khaoustov, Vladimir I.; Risin, Diana; Pellis, Neal R.; Yoffe, Boris
CS Department of Medicine, Veterans Affairs Medical Center, Baylor College of Medicine, Houston, TX, 77030, USA
SO In Vitro Cellular & Developmental Biology: Animal (2001), 37(2), 84-88 CODEN: IVCAED; ISSN: 1071-2690
PB Society for In Vitro Biology
DT Journal; General Review
LA English
AB A review with 18 refs. including the authors' own works. Developed at NASA, the rotary cell culture system (RCCS) allows the creation of unique microgravity environment of low shear force, high-mass transfer, and enables 3-dimensional (3D) cell culture of dissimilar cell types. Recently the authors demonstrated that a simulated microgravity is conducive for maintaining long-term cultures of functional hepatocytes and promote 3D cell assembly. Using DNA microarray technol., it is now possible to measure the levels of thousands of different messenger ribonucleic acids (mRNAs) in a single hybridization step. This technique is particularly powerful for comparing gene expression in the same tissue under different environmental conditions. The aim of this research was to analyze gene expression of hepatoblastoma cell line (HepG2) during early stage of 3D-cell assembly in simulated microgravity. For this, mRNA from HepG2 cultured in the RCCS was analyzed by DNA microarray. Analyses of HepG2 mRNA by 6K glass DNA microarray revealed changes in expression of 95 genes (overexpression of 85 genes and downregulation of 10 genes). The preliminary results indicated that ***simulated*** microgravity modifies the expression of several genes and that ***microarray*** technol. may provide new understanding of the fundamental biol. questions of how gravity affects the development and function of individual cells.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 371 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:331494 CAPLUS
DN 136:1284
TI The stanford microarray database

AU Sherlock, Gavin; Hernandez-Boussard, Tina; Kasarskis, Andrew; Binkley, Gail; Matese, John C.; Dwight, Selina S.; Kaloper, Miroslava; Weng, Shuai; Jin, Heng; Ball, Catherine A.; Eisen, Michael B.; Spellman, Paul T.; Brown, Patrick O.; Botstein, David; Cherry, J. Michael
CS Department of Genetics, Center for Clinical Sciences Research, Stanford University, Stanford, CA, 94305-5163, USA
SO Nucleic Acids Research (2001), 29(1), 152-155 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The Stanford Microarray Database (SMD) stores raw and normalized data from microarray expts., and provides web interfaces for researchers to retrieve, analyze and visualize their data. The two immediate goals for SMD are to serve as a storage site for microarray data from ongoing research at Stanford University, and to facilitate the public dissemination of that data once published, or released by the researcher. Of paramount importance is the connection of microarray data with the biol. data that pertains to the DNA deposited on the microarray (genes, clones etc.). SMD makes use of many public resources to connect expression information to the relevant biol., including SGD [Ball,C.A., Dolinski,K., Dwight,S.S., Harris,M.A., Issel-Tarver,L., Kasarskis,A., Scafe,C.R., Sherlock,G., Binkley,G., Jin,H. et al. (2000) Nucleic Acids Res., 28, 77-80], YPD and WormPD [Costanzo,M.C., Hogan,J.D., Cusick,M.E., Davis,B.P., Fancher,A.M., Hodges,P.E., Kondu,P., Lengieza,C., Lew-Smith,J.E., Lingner,C. et al. (2000) Nucleic Acids Res., 28, 73-76], Unigene [Wheeler,D.L., Chappey,C., Lash,A.E., Leipe,D.D., Madden,T.L., Schuler,G.D.,J Tatusova,T.A. and Rapp,B.A. (2000) Nucleic Acids Res., 28, 10-14], dbEST [Boguski,M.S., Lowe,T.M. and Tolstoshev,C.M. (1993) Nature Genet., 4, 332-333] and SWISS-PROT [Bairoch,A. and Apweiler,R. (2000) Nucleic Acids Res., 28, 45-48] and can be accessed at http://genome-www.stanford.edu/microarray.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 372 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:294318 CAPLUS
DN 136:1470
TI Target gene search for the metal-responsive transcription factor MTF-1
AU Lichtlen, P.; Wang, Y.; Belser, T.; Georgiev, O.; Certa, U.; Sack, R.; Schaffner, W.
CS Institute of Molecular Biology, University of Zurich, Zurich, CH-8057, Switz.
SO Nucleic Acids Research (2001), 29(7), 1514-1523 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB Activation of genes by heavy metals, notably zinc, cadmium and copper, depends on MTF-1, a unique zinc finger transcription factor conserved from insects to human. Knockout of MTF-1 in the mouse results in embryonic lethality due to liver decay, while knockout of its best characterized target genes, the stress-inducible metallothionein genes I and II, is viable, suggesting addnl. target genes of MTF-1. Here we report on a multi-pronged search for potential target genes of MTF-1, including ***microarray*** screening, SABRE selective amplification, a ***computer*** search for MREs (DNA-binding sites of MTF-1) and transfection of reporter genes driven by candidate gene promoters. Some new candidate target genes emerged, including those encoding .alpha.-fetoprotein, the liver-enriched transcription factor C/EBP.alpha.: and tear lipocalin/von Ebner's gland protein, all of which have a role in toxicity/the cell stress response. In contrast, expression of other cell stress-assocd. genes, such as those for superoxide dismutases, thioredoxin and heat shock proteins, do not appear to be affected by loss of MTF-1. Our expts. have also exposed some problems with target gene searches. First, finding the optimal time window for detecting MTF-1 target genes in a lethal phenotype of rapid liver decay proved problematical: 12.5-day-old mouse embryos (stage E12.5) yielded hardly any differentially expressed genes, whereas at stage 13.0 reduced expression of secretory liver proteins probably reflected the onset of liver decay, i.e. a secondary effect. Likewise, up-regulation of some proliferation-assocd. genes may also just reflect responses to the concomitant loss of 'hepatocytes. Another sobering finding concerns .gamma.-glutamylcysteine synthetase hc (.gamma.GCShc), which controls synthesis of the antioxidant glutathione and which was previously suggested to be a target gene contributing to the lethal phenotype in MTF-1 knockout mice. .gamma.-GCShc mRNA is reduced at the onset of liver decay but MTF-1 null mutant embryos manage to maintain a very high glutathione level until shortly before that stage, perhaps in an attempt to compensate for low expression of metallothioneins, which also have a role as antioxidants.
RE.CNT 65 THERE ARE 65 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 373 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:286100 CAPLUS
DN 135:353402
TI Recovering filter-based microarray data for pathways analysis using a multipoint alignment strategy
AU Reid, Robert; Dix, David J.; Miller, David; Krawetz, Stephen A.
CS Wayne State University School of Medicine, Detroit, MI, 48201, USA
SO BioTechniques (2001), 30(4), 762-764,766,768 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
AB The use of com. microarrays is rapidly becoming the method of choice for profiling gene expression and assessing various disease states. Research Genetics has provided a series of biol. and software tools to the research community for these analyses. The fidelity of data anal. using these tools is dependent on a series of well-defined ref. control points in the array. During the course of our investigations, it became apparent that in some instances the ref. control points that are required for anal. became lost in background noise. This effectively halted the anal. and the recovery of any information contained within that expt. To recover this data and to increase anal. veracity, the simple strategy of superimposing a template of ref. control points onto the exptl. array was developed. The utility of this tool is established in this communication.
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 374 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:266749 CAPLUS
DN 135:353397
TI Analysis of variance for gene expression microarray data
AU Kerr, M. Kathleen; Martin, Mitchell; Churchill, Gary A.
CS The Jackson Laboratory, Bar Harbor, ME, 04609, USA
SO Journal of Computational Biology (2000), 7(6), 819-837 CODEN: JCOBEM; ISSN: 1066-5277
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB Spotted cDNA microarrays are emerging as a powerful and cost-effective tool for large-scale anal. of gene expression. Microarrays can be used to measure the relative quantities of specific mRNAs in two or more tissue samples for thousands of genes simultaneously. While the power of this technol. has been recognized, many open questions remain about appropriate anal. of microarray data. One question is how to make valid ests. of the relative expression for genes that are not biased by ancillary sources of variation. Recognizing that there is inherent "noise" in microarray data, how does one est. the error variation assocd. with an estd. change in expression, i.e., how does one construct the error bars. The authors demonstrate that ANOVA methods can be used to normalize microarray data and provide ests. of changes in gene expression that are cor. for potential confounding effects. This approach establishes a framework for the general anal. and interpretation of microarray data.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 375 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:247543 CAPLUS
DN 134:276469
TI Methods and computer software products for multiple probe gene expression analysis
IN Ho, Ming-Hsiu
PA Affymetrix, Inc., USA
SO PCT Int. Appl., 75 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2001023614 A1 20010405 WO 2000-US26732 20000928 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG US 6505125 B1 20030107 US 2000-670510 20000926 AU 2000077309 A5 20010430 AU 2000-77309 20000928 US 2003216868 A1 20031120 US 2002-315923 20021209
PRAI US 1999-156353P P 19990928 US 2000-208956P P 20000531 US 2000-670510 A 20000926 WO 2000-US26732 W 20000928
AB Methods and computer software products are provided for analyzing gene expression data. In one embodiment, the expression of a gene is detd. by multiple probes in several expts. A principal component anal. is performed to obtain the relative expression of the gene in these expts.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 376 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:213808 CAPLUS
DN 136:1135
TI Design and on-chip synthesis technology of oligonucleotide microarray
AU Lu, Zuhong; Zhao, Yujie; He, Nongyao; Sun, Xiao
CS National Laboratory for Molecular and Biomolecular Electronics, Southeast University, Nanjing, 210096, Peop. Rep. China
SO Proceedings of SPIE-The International Society for Optical Engineering (2000), 4224(Biomedical Photonics and Optoelectronic Imaging), 118-121 CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal; General Review
LA English
AB A review, with refs., discussing genechip engineering including a set of techniques, such as chip fabrication, target gene prepn. and hybridization, pattern detection and processing, bioinformatics related to the probe design and data anal. Some results in on-chip synthesizing the oligonucleotides microarray with mol. stamping or microfluidic molds, and developing software for probe designs are presented.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 377 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN

AN 2001:168239 CAPLUS
DN 134:204717
TI Method and system for overlaying at least three microarray images to obtain a multicolor composite image
IN Stephan, Todd J.; Noblett, David A.; Yang, Jun
PA GSI Lumonics Life Science Trust, USA
SO PCT Int. Appl., 16 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2001016583 A2 20010308 WO 2000-US40806 20000901 W: CA, JP RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
PRAI US 1999-388204 A 19990901
AB Disclosed are a method and system for overlaying at least three microarray images to obtain a multicolor composite image, which is then displayed on a monitor of a computer system. The microarray images are taken from a microarray scanner of a DNA microarray and can be viewed simultaneously through the use of the image overlays where each image is represented by a different color. Each pixel of the composite image is generated by the OR operator applied to all corresponding pixels of the microarray images. Registration of the microarray images can be altered with a keyboard or mouse of the computer system.

L6 ANSWER 378 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:154070 CAPLUS
DN 135:237294
TI Experimental annotation of the human genome using microarray technology
AU Shoemaker, D. D.; Schadt, E. E.; Armour, C. D.; He, Y. D.; Garrett-Engele, P.; McDonagh, P. D.; Loerch, P. M.; Leonardson, A.; Lum, P. Y.; Cavet, G.; Wu, L. F.; Altschuler, S. J.; Edwards, S.; King, J.; Tsang, J. S.; Schimmack, G.; Schelter, J. M.; Koch, J.; Ziman, M.; Marton, M. J.; Li, B.; Cundiff, P.; Ward, T.; Castle, J.; Krolewski, M.; Meyer, M. R.; Mao, M.; Burchard, J.; Kidd, M. J.; Dal, H.; Phillips, J. W.; Linsley, P. S.; Stoughton, R.; Scherer, S.; Boguski, M. S.
CS Rosetta Inpharmatics, Inc., Kirkland, WA, 98034, USA
SO Nature (London, United Kingdom) (2001), 409(6822), 922-927 CODEN: NATUAS; ISSN: 0028-0836
PB Nature Publishing Group
DT Journal
LA English
AB The most important product of the sequencing of a genome is a complete, accurate catalog of genes and their products, primarily mRNA transcripts and their cognate proteins. Such a catalog cannot be constructed by computational annotation alone; it requires exptl. validation on a genome scale. Using 'exon' and 'tiling' arrays fabricated by ink-jet oligonucleotide synthesis, the authors devised an exptl. approach to validate and refine computational gene predictions and define full-length transcripts on the basis of co-regulated expression of their exons. These methods can provide more accurate gene nos. and allow the detection of mRNA splice variants and identification of the tissue- and disease-specific conditions under which genes are expressed. The authors apply the technique to chromosome 22q under 69 exptl. condition pairs, and to the entire human genome under two exptl. conditions. The authors discuss implications for more comprehensive, consistent and reliable genome annotation, more efficient, full-length complementary DNA cloning strategies and application to complex diseases.
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 379 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:136581 CAPLUS
DN 135:367311
TI Automation in microarray image analysis with AutoGene
AU Kuklin, Alexander; Shams, Soheil; Shah, Shishir
CS BioDiscovery, Inc., Los Angeles, CA, 90064, USA
SO JALA (2000), 5(5), 67-70 CODEN: JALLFO
PB JALA
DT Journal
LA English
AB AutoGene is a fully automated system that allows for batch processing of hundreds of images at a time and also incorporates more sophisticated image anal. and statistically reliable data quantification. The system has been designed to fully automate image anal. and data quantification operations and answer the need of the pharmaceutical drug discovery labs. and academic core facilities. Automatic spot finding is its main characteristic and autonomous operation the second. After quantification the data can be reviewed and shared by using a software ResultsReviewer.

L6 ANSWER 380 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:136580 CAPLUS
DN 135:367310
TI Tools for analyzing microarray expression data
AU Grewal, Anoop; Conway, Andrew
CS Silicon Genetics, Redwood City, CA, 94063, USA
SO JALA (2000), 5(5), 62-64 CODEN: JALLFO
PB JALA
DT Journal
LA English
AB Microarray technologies have emerged as key tools for genomic expression anal. for the purposes of studying disease states, identifying drug targets, and profiling time-, tissue- or stage-dependent changes. The resulting vol. of data generated necessitates the use of bioinformatics tools to find interesting gene expression patterns, to identify statistically significant changes across expts., and to provide addnl. tools relevant to data mining. We have developed a comprehensive workbench soln., GeneSpringTM, which (1) comes with an intuitive interface incorporating organized file management, (2) handles data from multiple array formats, (3) includes multiple data display formats, (4) includes a suite of statistical clustering tools, and (5) incorporates automated annotation and cross-referencing. We will discuss the set of algorithms collectively designed to facilitate gene function identification from large scale genomic expression expts.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 381 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:104773 CAPLUS
DN 134:142365
TI "Gene switch" found with the computer
AU Grote, Korbinian
CS Institut Saugetiergenetik, GSF - Forschungszentrum Umwelt Gesundheit GmbH, Neuherberg, 85758, Germany
SO Bioforum (2000), 23(6), 404-405 CODEN: BFRME3; ISSN: 0940-0079
PB GIT Verlag GmbH
DT Journal; General Review
LA German
AB A brief review with 5 refs., describing transcription complex of the genome, detection of single binding sites in the genome, and research on structure of regulatory networks and participation of disease-relevant genes within transcription cascades. Detection of complex promoter structures and single bindings sites by ***computer*** models and application of ***microarray*** technol. for anal. of gene expression are discussed.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 382 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:62258 CAPLUS
DN 137:89385
TI The microarray explorer tool for data mining of cDNA microarrays: application for the mammary gland. [Erratum to document cited in CA135:29797]
AU Lemkin, Peter F.; Thornwall, Gregory C.; Walton, Katherine D.; Hennighausen, Lothar
CS Laboratory of Experimental and Computational Biology, Frederick, MD, 21702, USA
SO Nucleic Acids Research (2000), 28(24), No pp. given CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB In the last line of the Abstr., the Web address for MAExplorer is incorrect; the correct address should be http://www.lecb.ncifcrf.gov/MAExp lorer.

L6 ANSWER 383 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:38172 CAPLUS
DN 134:265844
TI MAD: a suite of tools for microarray data management and processing
AU Liao, Birong; Hale, Walker; Epstein, Charles B.; Butow, Ronald A.; Garner, Harold R.
CS Center for Biomedical Inventions, University of Texas Southwestern Medical Center, Dallas, TX, 75390, USA
SO Bioinformatics (2000), 16(10), 946-947 CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
AB Microarray data management and processing (MAD) is a set of Windows integrated software for microarray anal. It consists of a relational database for data storage with many user-interfaces for data manipulation, several text file parsers and Microsoft Excel macros for automation of data processing, and a generator to produce text files that are ready for cluster anal.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 384 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:843644 CAPLUS
DN 135:29797
TI The Microarray Explorer tool for data mining of cDNA microarrays: application for the mammary gland
AU Lemkin, Peter F.; Thornwall, Gregory C.; Walton, Katherine D.; Hennighausen, Lothar
CS Laboratory of Experimental and Computational Biology, NCI, FCRDC, Frederick, MD, 21702, USA
SO Nucleic Acids Research (2000), 28(22), 4452-4459 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The Microarray Explorer (MAExplorer) is a versatile Java-based data mining bioinformatic tool for analyzing quant. cDNA expression profiles across multiple microarray platforms and DNA labeling systems. It may be run as either a stand-alone application or as a Web browser apple over the Internet. With this program it is possible to (i) analyze the expression of individual genes, (ii) analyze the expression of gene families and clusters, (iii) compare expression patterns and (iv) directly access other genomic databases for clones of interest. Data may be downloaded as required

from a Web server or in the case of the stand-alone version, reside on the user's computer. Analyses are performed in real-time and may be viewed and directly manipulated in images, reports, scatter plots, histograms, expression profile plots and cluster analyses plots. A key feature is the clone data filter for constraining a working set of clones to those passing a variety of user-specified logical and statistical tests. Reports may be generated with hypertext Web access to UniGene, GenBank and other Internet databases for sets of clones found to be of interest. Users may save their explorations on the Web server or local computer and later recall or share them with other scientists in this groupware Web environment. The emphasis on direct manipulation of clones and sets of clones in graphics and tables provides a high level of interaction with the data, making it easier for investigators to test ideas when looking for patterns. The MAExplorer was used to profile gene expression patterns of 1500 duplicated genes isolated from mouse mammary tissue. The authors identified genes that are preferentially expressed during pregnancy and during lactation. One gene we identified, carbonic anhydrase III, is highly expressed in mammary tissue from virgin and pregnant mice and in gene knock-out mice with underdeveloped mammary epithelium. Other genes, which include those encoding milk proteins, are preferentially expressed during lactation. MAExplorer may be accessed at http://www.lecb.ncifcrf.gov.MAExplorer.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 385 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:783946 CAPLUS
DN 135:117868
TI General nonlinear framework for the analysis of gene interaction via multivariate expression arrays
AU Kim, Seungchan; Dougherty, Edward R.; Bittner, Michael L.; Chen, Yidong; Sivakumar, Krishnamoorthy; Meltzer, Paul; Trent, Jeffrey M.
CS Department of Electrical Engineering, Texas A&M University, College Station, TX, 77843-3128, USA
SO Journal of Biomedical Optics (2000), 5(4), 411-424 CODEN: JBOPFO; ISSN: 1083-3668
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
AB A cDNA microarray is a complex biochem.-optical system whose purpose is the simultaneous measurement of gene expression for thousands of genes. In this paper the authors propose a general statistical approach to finding assocns. between the expression patterns of genes via the coeff. of detn. This coeff. measures the degree to which the transcriptional levels of an obsd. gene set can be used to improve the prediction of the transcriptional state of a target gene relative to the best possible prediction in the absence of observations. The method allows incorporation of knowledge of other conditions relevant to the prediction, such as the application of particular stimuli or the presence of inactivating gene mutations, as predictive elements affecting the expression level of a given gene. Various aspects of the method are discussed: prediction quantification, unconstrained prediction, constrained prediction using ternary perceptrons, and design of predictors given small nos. of replicated microarrays. The method is applied to a set of genes under-going genotoxic stress for validation according to the manner in which it points toward previously known and unknown relationships. The entire procedure is supported by software that can be applied to large gene sets, has a no. of facilities to simplify data anal., and provides graphics for visualizing exptl. data, multiple gene interaction, and prediction logic.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 386 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:773973 CAPLUS
DN 135:102920
TI High throughput and global approaches to gene expression
AU Ghosh, David
CS Institute for Transcriptional Informatics, Pittsburgh, PA, 15230, USA
SO Combinatorial Chemistry and High Throughput Screening (2000), 3(5), 411-420 CODEN: CCHSFU; ISSN: 1386-2073
PB Bentham Science Publishers
DT Journal; General Review
LA English
AB A review with 79 refs. In the past several years, a new set of technologies based on whole genome anal. have revolutionized the study of gene expression. These microarray or "gene chip" technologies, which arose out of the development of large-scale sequencing approaches, are now coming into increasing use, generating a far greater vol. of data than the data representing the sequences themselves. This review focuses on the current state of development of these technologies, and the available approaches to manage and analyze the information they generate. The applicability of this technol. to general problems in biomedicine is also discussed.
RE.CNT 79 THERE ARE 79 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 387 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:688262 CAPLUS
DN 133:277141
TI Microarrays of ESTs for monitoring multiple gene expression in filamentous fungi
IN Berka, Randy M.; Rey, Michael W.; Shuster, Jeffrey R.; Kauppinen, Sakari; Clausen, Ib Groth; Olsen, Peter Bjarke
PA Novo Nordisk Biotech, Inc., USA; Novo Nordisk A/S
SO PCT Int. Appl., 3161 pp. CODEN: PIXXD2
DT Patent
LA English

FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2000056762 A2 20000928 WO 2000-US7781 20000322 WO 2000056762 A3 20020711 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG AU 2000039154 A5 20001009 AU 2000-39154 20000322 EP 1235855 A2 20020904 EP 2000-918323 20000322 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY
PRAI US 1999-273623 A 19990322 WO 2000-US7781 W 20000322
AB The present invention relates to methods for monitoring differential expression of a plurality of genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells using microarrays contg. filamentous fungal expressed sequenced tags. The present invention also relates to filamentous fungal expressed sequenced tags and to computer readable media and substrates contg. such expressed sequenced tags for monitoring expression of a plurality of genes in filamentous fungal cells. DNA sequences are provided for 3770 ESTs from Fusarium venenatum, 606 ESTs from Aspergillus niger, 4024 ESTs from Aspergillus oryzae, and 459 ESTs from Trichoderma reesei.

L6 ANSWER 388 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:670670 CAPLUS
DN 135:884
TI Computational simulation of bio-microfluidic processes in integrated DNA biochips
AU Przekwas, A.; Makhijani, V.; Athavale, M.; Klein, A.; Bartsch, P.
CS CFD Research Corp, Huntsville, AL, USA
SO Micro Total Analysis Systems 2000, Proceedings of the .mu.TAS Symposium, 4th, Enschede, Netherlands, May 14-18, 2000 (2000), 561-564. Editor(s): Van den Berg, Albert; Olthuis, W.; Bergveld, Piet. Publisher: Kluwer Academic Publishers, Dordrecht, Neth. CODEN: 69AJPB
DT Conference
LA English
AB Recent developments in mol. biol. and genetic anal. have inspired strong interests in miniaturization of DNA anal. on a single microfluidic chip. In the last few years there has been tremendous interest in developing a complete biochem. intelligent microsystem for extn., concn., amplification, anal., and processing of DNA. Current biochips are being developed in a very conventional exptl. trial and error manner with little computational design support. This paper presents a new software tool, CFD-ACE+, which has been developed for multidisciplinary, multiscale design of biochips. The paper describes the computational physics involved in modeling bio-microfluidic devices, and demonstrates it on a biochip for extn., concn. of DNA from fluidic samples and on PCR amplification. Other bioprocessing steps such as hybridization and electrophoretic sepn. in microfluidic networks on a chip, can also be analyzed with CFD-ACE+.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 389 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:606500 CAPLUS
DN 133:256027
TI Gradient gas sensor microarrays for on-line process control - a new dynamic classification model for fast and reliable air quality assessment
AU Menzel, R.; Goschnick, J.
CS Forschungszentrum Karlsruhe, Institut fur Instrumentelle Analytik, Karlsruhe, D-76021, Germany
SO Sensors and Actuators, B: Chemical (2000), B68(1-3), 115-122 CODEN: SABCEB; ISSN: 0925-4005
PB Elsevier Science S.A.
DT Journal
LA English
AB A dynamic gas classification model was developed to achieve a reliable online discrimination at very fast response times. The aim was to be able to follow rapid changes in gas compns. using an electronic nose in consumer applications. The electronic nose is based on a micro-array specially designed for prodn. at very low costs. This is essential for application in mass products. Common classification methods used for signal evaluation of electronic noses such as linear discriminant anal. (LDA), neural networks (NN), or soft independent modeling of class analogy (SIMCA) failed to detect non-stationary gas mixts. However, the new model combines classification of steady states with transient evaluation via time series anal. Rapid signal transients are detected by appropriate digital filters; steady state signals are classified by the above mentioned std. methods. The simplicity of the algorithm model allows implementation in low-cost electronic units, contg. micro-controllers with very limited memory capacity. To give an example, the automatic control of the ventilation flap of automobiles was studied. Intermediate streams of bad air could be detected within 1-2 s. The error of pollutant detection was reduced from 25%, applying static classification only, to 10% for the new dynamic model.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 390 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:521379 CAPLUS
DN 133:217973
TI Thyroid hormone regulation of hepatic genes in Vivo detected by complementary DNA microarray
AU Feng, Xu; Jiang, Yuan; Meltzer, Paul; Yen, Paul M.

CS Molecular Regulation and Neuroendocrinology Section Clinical Endocrinology Branch, National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health, Bethesda, MD, 20892, USA
SO Molecular Endocrinology (2000), 14(7), 947-955 CODEN: MOENEN; ISSN: 0888-8809
PB Endocrine Society
DT Journal
LA English
AB The liver is an important target organ of thyroid hormone. However, only a limited no. of hepatic target genes have been identified, and little is known about the pattern of their regulation by thyroid hormone. We used a quant. fluorescent cDNA microarray to identify novel hepatic genes regulated by thyroid hormone. Fluorescent-labeled cDNA prepd. from hepatic RNA of T3-treated and hypothyroid mice was hybridized to a cDNA ***microarray*** , representing 2225 different mouse genes, followed by ***computer*** anal. to compare relative changes in gene expression. Fifty five genes, 45 not previously known to be thyroid hormone-responsive genes, were found to be regulated by thyroid hormone. Among them, 14 were pos. regulated by thyroid hormone, and unexpectedly, 41 were neg. regulated. The expression of 8 of these genes was confirmed by Northern blot analyses. Thyroid hormone affected gene expression for a diverse range of cellular pathways and functions, including gluconeogenesis, lipogenesis, insulin signaling, adenylate cyclase signaling, cell proliferation, and apoptosis. This is the first application of the microarray technique to study hormonal regulation of gene expression in vivo and should prove to be a powerful tool for future studies of hormone and drug action.
RE.CNT 69 THERE ARE 69 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 391 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:494493 CAPLUS
DN 133:359695
TI Genome-wide characterization of the Zap1p zinc-responsive regulon in yeast
AU Lyons, Thomas J.; Gasch, Audrey P.; Gaither, L. Alex; Botstein, David; Brown, Patrick.O.; Eide, David J.
CS Department of Nutritional Sciences, University of Missouri, Columbia, MO, 65211, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2000), 97(14), 7957-7962 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB The Zap1p transcription factor senses cellular zinc status and increases expression of its target genes in response to zinc deficiency. Previously known Zap1p-regulated genes encode the Zrt1p, Zrt2p, and Zrt3p zinc transporter genes and Zap1p itself. To allow the characterization of addnl. genes in yeast important for zinc homeostasis, a systematic study of gene expression on the genome-wide scale was used to identify other Zap1p target genes. Using a combination of DNA ***microarrays*** and a ***computer*** -assisted anal. of shared motifs in the promoters of similarly regulated genes, we identified 46 genes that are potentially regulated by Zap1p. Zap1p-regulated expression of seven of these newly identified target genes was confirmed independently by using lacZ reporter fusions, suggesting that many of the remaining candidate genes are also Zap1p targets. Our studies demonstrate the efficacy of this combined approach to define the regulon of a specific eukaryotic transcription factor.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 392 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:431076 CAPLUS
DN 133:306055
TI Genome-directed primers for selective labeling of bacterial transcripts for DNA microarray analysis
AU Talaat, Adel M.; Hunter, Preston; Johnston, Stephen Albert
CS Center for Biomedical Inventions and Departmtent of Medicine, University of Texas-Southwestern Medical Center, Dallas, TX, 75390-8573, USA
SO Nature Biotechnology (2000), 18(6), 679-682 CODEN: NABIF9; ISSN: 1087-0156
PB Nature America Inc.
DT Journal
LA English
AB DNA microarrays have the ability to analyze the expression of thousands of the same set of genes under at least two different exptl. conditions. However, DNA microarrays require substantial amts. of RNA to generate the probes, esp. when bacterial RNA is used for hybridization (50 .mu.g of bacterial total RNA contains approx. 2 .mu.g of mRNA). We have developed a computer-based algorithm for prediction of the minimal no. of primers to specifically anneal to all genes in a given genome. The algorithm predicts, for example, that 37 oligonucleotides should prime all genes in the Mycobacterium tuberculosis genome. We tested the usefulness of the genome-directed primers (GDPs) in comparison to random primers for gene expression profiling using DNA microarrays. Both types of primers were used to generate fluorescent-labeled probes and to hybridize to an array of 960 mycobacterial genes. Compared to random-primer probes, the GDP probes were more sensitive and more specific, esp. when mammalian RNA samples were spiked with mycobacterial RNA. The GDPs were used for gene expression profiling of mycobacterial cultures grown to early log or stationary growth phases. This approach could be useful for accurate genome-wide expression anal., esp. for in vivo gene expression profiling, as well as directed amplification of sequenced genomes.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 393 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:417804 CAPLUS
DN 134:173817
TI A ***computer*** program for generating gene-specific fragments for ***microarrays***
AU Xu, Dong; Xu, Ying; Li, Gary; Zhou, Jizhong
CS Computational Biosciences Section, Oak Ridge National Laboratory, Oak Ridge, TN, 37831, USA
SO Frontiers Science Series (2000), 30(Currents in Computational Molecular Biology), 3-4 CODEN: FCFUEO; ISSN: 0915-8502
PB Universal Academy Press, Inc.
DT Journal
LA English
AB A computer program useful in selecting geno-specific fragment which can be used to design PCR primer pairs for PCR amplification and arrays was developed.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 394 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:333916 CAPLUS
DN 134:142403
TI Automated analysis of multivariate nonlinear gene relations based on cDNA microarray expression data
AU Kim, Seungchan; Dougherty, Edward R.; Bittner, Michael L.; Chen, Yidong; Sivakumar, Krishnamoorthy; Meltzer, Paul S.; Trent, Jeffrey M.
CS Dep. Electr. Eng., Texas A&M Univ., USA
SO Proceedings of SPIE-The International Society for Optical Engineering (2000), 3926(Advances in Nucleic Acid and Protein Analyses, Manipulation, and Sequencing), 150-155 CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
AB A cDNA microarray is a complex biochem.-optical system whose purpose is the simultaneous measurement of gene expression for thousands of genes. This paper describes a general statistical environment for finding assocns. among gene expression patterns, and between genes and external conditions, via the coeff. of detn. This coeff. measures the degree to which the transcriptional levels of an obsd. gene set can be used to improve the prediction of the transcriptional state of a target gene relative to the best possible prediction in the absence of observations. Various aspects of the method are discussed: prediction quantification, design of predictors given small nos. of replicated microarrays, and constrained prediction using ternary perceptrons. A main focus is the supporting software and its facilities for data anal. and visualization.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 395 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:263599 CAPLUS
DN 133:160266
TI Overview of a microarray scanner: design essentials for an integrated acquisition and analysis platform
AU Basarsky, Trent; Verdnik, Damian; Zhai, Jack Ye; Wellis, David
CS Axon Instruments, Inc., Foster City, CA, USA
SO Microarray Biochip Technology (2000), 265-284. Editor(s): Schena, Mark. Publisher: Eaton Publishing Co., Natick, Mass. CODEN: 68VMAZ
DT Conference; General Review
LA English
AB A review with 15 refs. Data quality form hardware and data anal. and confidence measure from software form the basis of a well designed microarray scanner and data extn. software system. Successful hardware design is only possible if one has a deep understanding and experience of optical and electronic technologies, whereas the usability and efficiency of such a system is derived form the tightly integrated communication between hardware and software, including optimized algorithms and and a thoughtful and easy to use software interface. The final requirement of cost can be met by offering the scanner and multiple copies of the acquisition and anal. software at a value price point attractive to both academia an industry, as accomplished with the GenePix 4000. The future of microarray scanning and anal. can be summarized in one word: automation. On the software side, there is not yet an anal. package that can ext. the data from a microarray without human intervention, but existing software is rapidly approaching this point. Anal. of dataset from multiple arrays is already offered, but not as a component of a completely integrated system. On both the hardware and software sides, full automation is not far off for integrated scanning and anal. systems.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 396 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:250157 CAPLUS
DN 133:203782
TI Principal components analysis to summarize microarray experiments: Application to sporulation time series
AU Raychaudhuri, Soumya; Stuart, Joshua M.; Altman, Russ B.
CS Stanford Medical Informatics, Stanford University, Stanford, CA, 94305-5479, USA
SO Pacific Symposium on Biocomputing 2000, Honolulu, Jan 4-9, 2000 (2000), 455-466. Editor(s): Altman, Russ B. Publisher: World Scientific Publishing Co. Pte. Ltd., Singapore, Singapore. CODEN: 68UQA8
DT Conference
LA English
AB A series of microarray expts. produces observations of differential expression for thousands of genes across multiple conditions. It is often not clear whether a set of expts. are measuring fundamentally different gene expression states or are measuring

similar states created through different mechanisms. It is useful, therefore, to define a core set of independent features for the expression states that allow them to be compared directly. Principal components anal. (PCA) is a statistical technique for detg. the key variables in a multidimensional data set that explain the differences in the observations, and can be used to simplify the anal. and visualization of multidimensional data sets. The authors show that application of PCA to expression data (where the exptl. conditions are the variables, and the gene expression measurements are the observations) allows us to summarize the ways in which gene responses vary under different conditions. Examn. of the components also provides insight into the underlying factors that are measured in the expts. The authors applied PCA to the publicly released yeast sporulation data set (Chu et al. 1998). In that work, 7 different measurements of gene expression were made over time. PCA on the time-points suggests that much of the obsd. variability in the expt. can be summarized in just 2 components-i.e. 2 variables capture most of the information. These components appear to represent (1) overall induction level and (2) change in induction level over time. The authors also examd. the clusters proposed in the original paper, and show how they are manifested in principal component space. These results are available on the internet at http://www.smi.stanford.edu/projects/helix/PCArray.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 397 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:192935 CAPLUS
DN 132:290586
TI Making the most of microarray data
AU Gaasterland, Terry; Bekiranov, Stefan
CS Laboratory of Computational Genomics, The Rockefeller University, New York, NY, 10021, USA
SO Nature Genetics (2000), 24(3), 204-206 CODEN: NGENEC; ISSN: 1061-4036
PB Nature America
DT Journal; General Review
LA English
AB The title research of Brown, M.P.S. et al (Proc. Nat'l. Acad. Sci., U.S.A., 2000, 97, pg. 262-267) is reviewed with commentary and 6 refs. The impact of microarray technol. on biol. will depend on computational methods of data anal. A supervised computer-learning method using support vector machines predicts gene function from expression data-and shows promise.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 398 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:80222 CAPLUS
DN 133:115617
TI Development of an efficient data processing method for cDNA microarray and its application to tissue expression profiling
AU Kadota, Koji; Miki, Rika; Okazaki, Yasushi; Shimizu, Kentaro; Hayashizaki, Yoshihide
CS Genome Science Lab, Genomic Sciences Center, Ibaraki, 305-0074, Japan
SO Genome Informatics Series (1999), 10, 221-222 CODEN: GINSE9; ISSN: 0919-9454
PB Universal Academy Press
DT Journal
LA English
AB The authors report the development of a filtering program to selectively ext. genes expressed in cDNA microarrays. Probe (tissue mRNA) were prepd. by labeling Cy-3 dye. The cDNA microarray uses the dual dye system. The authors used Cy-5 labeled embryo 17.5 days (whole body) as ref. The algorithm of this filtering program consists of 3 steps: (1) omit the results which have flags (flags are built manually when the spot image does not fulfill a certain criteria), (2) eliminate spots whose signal intensity is less than mean (background signal) + 3.sigma. in both Cy-3 and Cy-5, (3) eliminate spots that are located outside the best fit line (least-mean squares). This program was applied for the anal. of full-length RIKEN cDNA 20K microarray and analyzed the expression profile of normal adult and embryonic tissues.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 399 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:38505 CAPLUS
DN 132:217619
TI Knowledge-based analysis of microarray gene expression data by using support vector machines
AU Brown, Michael P. S.; Grundy, William Noble; Lin, David; Cristianini, Nello; Sugnet, Charles Walsh; Furey, Terrence S.; Ares, Manuel, Jr.; Haussler, David
CS Department of Computer Science and Department of Biology, University of California, Santa Cruz, Santa Cruz, CA, 95064, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2000), 97(1), 262-267 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB We introduce a method of functionally classifying genes by using gene expression data from DNA microarray hybridization expts. The method is based on the theory of support vector machines (SVMs). SVMs are considered a supervised computer learning method because they exploit prior knowledge of gene function to identify unknown genes of similar function from expression data. SVMs avoid several problems assocd. with unsupervised clustering methods, such as hierarchical clustering and self-organizing maps. SVMs have many math. features that make them attractive for gene expression anal., including their flexibility in choosing a similarity function, sparseness of soln. when dealing with large data sets, the ability to handle large feature spaces, and the ability to identify outliers. We test several SVMs that use different similarity metrics, as well as some other supervised learning methods, and find that the SVMs best identify sets of genes with a common function using expression data. Finally, we use SVMs to predict functional roles for uncharacterized yeast ORFs based on their expression data.
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 400 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1999:551900 CAPLUS
DN 131:194891
TI Present status and problems of DNA microarray informatics
AU Eguchi, Yukihiro
CS Res. Inst., Mitsui Knowledge Ind. Co., Ltd., Japan
SO Jikken Igaku (1999), 17(13), 1670-1673 CODEN: JIIGEF; ISSN: 0288-5514
PB Yodosha
DT Journal; General Review
LA Japanese
AB A review with 10 refs., on the data management and anal. for gene expression profiles produced by DNA microarray technol. Computer software and information systems for the anal. of large-scale expression data, cluster anal., and identification of genetic network are discussed.

L6 ANSWER 401 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1999:53123 CAPLUS
DN 130:247491
TI Options available - from start to finish - for obtaining expression data by microarray
AU Bowtell, David D. L.
CS Peter MacCallum Cancer Institute, Melbourne, 3000, Australia
SO Nature Genetics (1999), 21(1, Suppl.), 25-32 CODEN: NGENEC; ISSN: 1061-4036
PB Nature America
DT Journal; General Review
LA English
AB A review, with 35 refs. The excitement surrounding microarray technol. has been tempered by the limited ability of the general biomedical research community to gain access to it. Given that the hardware required for exploitation of the technol. is becoming increasingly available, it is an appropriate moment to review options, be they com. or publically available. Here, a snapshot is provided of the rapidly changing field of microarray-based RNA expression anal. and the components and procedures for putting together a complete system are considered. The complete system is divided into sample prepn., array generation and sample anal., and data handling and interpretation.
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 402 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1998:455089 CAPLUS
DN 129:171114
TI Adapting the Biomek 2000 Laboratory Automation Workstation for printing DNA microarrays
AU Macas, Jiri; Nouzova, Marcela; Galbraith, David W.
CS Univ. Arizona, Tucson, AZ, USA
SO BioTechniques (1998), 25(1), 106, 108-110 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
AB The Biomek 2000 Lab. Automation Workstation is used for liq. handling and other repetitive operations in many labs. Since it has very good spatial positioning capabilities, we have modified this workstation to deliver samples at high densities onto microscope slides to produce DNA microarrays. The workstation tool, originally designed for bacterial colony replication, was adapted to carry special printing pins and was further modified to improve its positional accuracy. Software written in the Tool Command Language was concurrently developed to control the movements of the workstation arm during the process of printing. With these modifications, the workstation can reliably deliver individual samples at a spacing of 0.5 mm, corresponding to a total of more than 3000 samples on a single slide. Arrays prepd. in this way were successfully tested in hybridization expts.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 403 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1996:445602 CAPLUS
DN 125:179671
TI Application of the finite analytic numerical method. Part 1. Diffusion problems on coplanar and elevated interdigitated microarray band electrodes
AU Jin, Baokang; Qian, Weijun; Zhang, Zuxun; Shi, Hansheng
CS Department of Chemistry and National Key Laboratory of Coordination Chemistry, Nanjing University, Nanjing, 210093, Peop. Rep. China
SO Journal of Electroanalytical Chemistry (1996), 411(1-2), 29-36 CODEN: JECHES; ISSN: 0368-1874
PB Elsevier
DT Journal
LA English
AB Diffusion problems on coplanar and elevated interdigitated microarray band electrodes (IDAs) were studied by the finite analytic numerical method (FAM). Chronoamperometric curves and steady-state current-potential curves for both coplanar and elevated IDAs were simulated for diffusion controlled and quasi-reversible systems. The simulated results for coplanar IDAs were compared with those available

in the literature, and are in good agreement. The influence of the geometric parameters (electrode height he, ratio of electrode width we and gap width wg) of the elevated IDAs were also studied. The computing time necessary is much less compared with results in the literature.

L6 ANSWER 404 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1991:666274 CAPLUS
DN 115:266274
TI Computer generated microlens arrays and their application to optical free space switching networks
AU Bird, K. D.; Daly, D.; Hall, T. J.
CS King's Coll., London, UK
SO IEE Conference Publication (1991), 342(Int. Conf. Hologr. Syst., Compon. Appl., 3rd, 1991), 57-61 CODEN: IECPB4; ISSN: 0537-9989
DT Journal
LA English
AB The application of microlens arrays into optical switching architectures is addressed. The diffractive and refractive properties of microlens arrays were demonstrated in their use as efficient optical fan-in/fan-out array generators in the Fourier and image plane resp. A flexible and scalable approach to the generation of these lens arrays of high quality and uniformity has been detailed. Characterization of HOECHST AZ4620A resist has resulted in the photolithog. prodn. of multilevel structures of approximated lens profiles, allowing future control of f-nos. and aberrations. This may also be extended to the fabrication of surface relief structures for use as alternative fan-out array generators. Future research is into the control of these lenses during annealing, their optical qualities and subsequently the integration of optical fibers to lens waveguides in switching architectures. Initial insight into the tolerances in design are presented.

L6 ANSWER 405 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1990:107213 CAPLUS
DN 112:107213
TI Passivation of pinholes in octadecanethiol monolayers on gold electrodes by electrochemical polymerization of phenol
AU Finklea, Harry O.; Snider, Daniel A.; Fedyk, John
CS Dep. Chem., West Virginia Univ., Morgantown, WV, 26506-6045, USA
SO Langmuir (1990), 6(2), 371-6 CODEN: LANGD5; ISSN: 0743-7463
DT Journal
LA English
AB An organized monolayer of octadecanethiol on a Au electrode strongly inhibits faradaic reactions except at pinholes in the monolayer. For simpler outer-sphere redox couples, the monolayer-coated electrode behaves like a microelectrode array, with pinholes acting as the microelectrodes. The av. size and sepn. of the pinholes can be estd. by fitting the exptl. cyclic voltammograms with ***simulated*** voltammograms for a ***microarray*** electrode. The pinholes are selectively and permanently passivated by electrochem. polymn. of phenol in dil. sulfuric acid. The deposition of poly(phenylene oxide) suppresses the pinhole currents at low overpotential, but residual faradaic currents become visible at large overpotential. The residual currents are assigned to electron tunneling between the electrode and mols. which partially penetrate the monolayer.

L6 ANSWER 406 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1989:162368 CAPLUS
DN 110:162368
TI Time and spatial dependence of the concentration of less than 105 microelectrode-generated molecules
AU Licht, Stuart; Cammarata, Vince; Wrighton, Mark S.
CS Dep. Chem., Massachusetts Inst. Technol., Cambridge, MA, 02139, USA
SO Science (Washington, DC, United States) (1989), 243(4895), 1176-8 CODEN: SCIEAS; ISSN: 0036-8075
DT Journal
LA English
AB The time and spatial dependence of the concn. of as few as 40,000 electrogenerated, redox-active mols. was detd. The distance between generator and detector microelectrodes in an array used in the study could be varied from 0.8 to 28 .mu.m. Measurements of a sufficiently small ensemble of mols. allowed the exptl. results to be compared with a quant. simulation of the random movement of each member of the ensemble. The transit time of an electrogenerated species from the generator to a collector microelectrode was measured as a function of viscosity, diffusivity, and distance.

L6 ANSWER 407 OF 407 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1985:413455 CAPLUS
DN 103:13455
TI Numerical ***simulation*** of convective diffusion at a ***microarray*** channel electrode
AU Moldoveanu, S.; Anderson, J. L.
CS Dep. Chem., Univ. Georgia, Athens, GA, 30602, USA
SO Journal of Electroanalytical Chemistry and Interfacial Electrochemistry (1985), 185(2), 239-52 CODEN: JEIEBC; ISSN: 0022-0728
DT Journal
LA English
AB Concn. profiles and currents were stimulated for an array electrode on one wall of a rectangular flow-through channel, using the backward implicit finite difference numerical procedure to solve the equation governing the convective diffusion process. Different simplifying hypotheses usually considered in these types of calcns., and their concomitant errors were analyzed. A simple criterion for estg. the importance of longitudinal and lateral diffusion was developed. The responses of a variety of both regular and pseudo-randomly distributed geometries of array electrodes were evaluated under a wide range of conditions. Current response was evaluated as a function of the no. of active sites, fractional surface blockage, and flow conditions, relative to solid electrodes. The geometrical pattern of the array was found to affect the current response, a regularly spaced array yielding the max. response for a given degree of partial blockage of the electrode and a const. no. of microelectrodes.

=> d his
(FILE 'HOME' ENTERED AT 18:48:15 ON 19 JUN 2006)
FILE 'CAPLUS' ENTERED AT 18:48:28 ON 19 JUN 2006
L1 341 S (SIMULAT?(10A)(MICROARRAY# OR (MICRO(W)ARRAY#)))/BI,AB
L2 641 S (COMPUTER?(10A)(MICROARRAY# OR (MICRO(W)ARRAY#)))/BI,AB
L3 929 S L1 OR L2
L4 859 S L3 NOT 2006/PY
L5 611 S L4 NOT 2005/PY
L6 407 S L5 NOT 2004/PY

=> log y

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
ENTRY SESSION		
FULL ESTIMATED COST	1136.25	1136.46

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
ENTRY SESSION		
CA SUBSCRIBER PRICE	-296.25	-296.25

STN INTERNATIONAL LOGOFF AT 18:52:25 ON 19 JUN 2006